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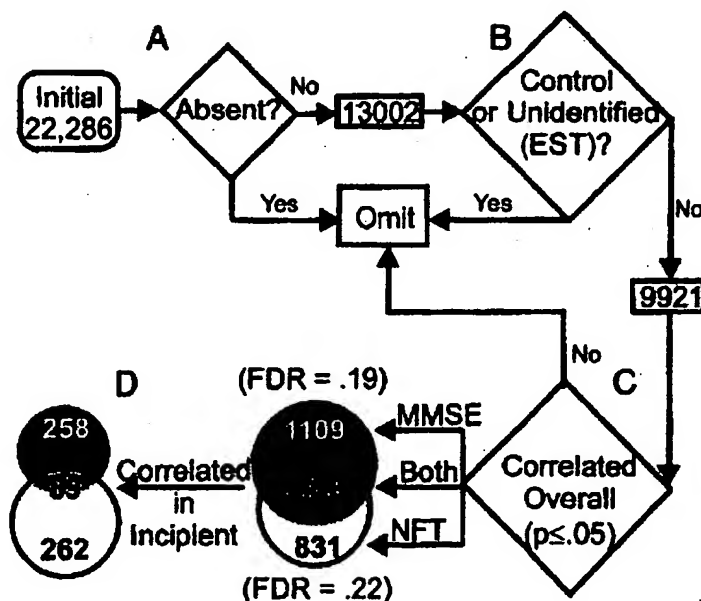
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(54) Title: ASSAY AND METHOD FOR DIAGNOSING AND TREATING ALZHEIMER'S DISEASE



(57) Abstract: Methods and kits for diagnosing Alzheimer's disease and/or incipient Alzheimer's disease are disclosed. The methods and kits of the invention utilize a set of genes and their encoded proteins that are shown to be correlated with incipient Alzheimer's disease.

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Assay and Method for Diagnosing and Treating Alzheimer's Disease

Related Applications

This application claims priority from provisional application Serial No. 60/542,281, filed February 9, 2004, incorporated herein in its entirety.

Field of the Invention

The invention relates to assays and methods for diagnosing and treating Alzheimer's disease (AD). More particularly, this invention relates to methods for detecting changes in the pattern of gene expression that correlated with AD, and in particular, with incipient AD, and using these changes to either diagnose AD in a patient or screen compounds for treating AD.

Background of the Invention

Alzheimer's disease (AD) has received intense study during the past decades. Multiple processes have been implicated in AD, notably including abnormal beta-amyloid production, tau hyperphosphorylation and neurofibrillary tangles (NFTs), synaptic pathology, oxidative stress, inflammation, protein processing or misfolding, calcium dyshomeostasis, aberrant reentry of neurons into the cell cycle, cholesterol synthesis, and effects of hormones or growth factors. Nevertheless, the pathogenic factors that initiate these processes remain elusive.

Several reasons account for the substantial resistance of AD pathogenesis to analysis. One is the vast extent and complexity of the disease, which affects numerous molecules, cells, and biochemical pathways. Another is that clinically normal subjects may exhibit considerable AD pathology, blurring criteria for distinguishing subjects with normal aging, mild cognitive impairment, or incipient AD or progressive AD.

- 1 -

Thus, there is a need for an assay that enables the medical practitioner to distinguish these conditions.

Summary of the Invention

In one aspect of the invention there is provided an oligonucleotide or cDNA array comprising a solid support comprising a plurality of different oligonucleotide probes or cDNA probes, each oligonucleotide probe or cDNA specific for a gene listed in Table 6, Table 5 or Table 4. In another aspect of the invention there is provided a kit comprising an oligonucleotide array of the invention and a reagent. In another aspect there is provided an array with a plurality of probes for measuring proteins encoded by the genes listed in Tables 6, 5 or 4.

In another aspect of the invention there is provided a method of detecting in a body sample of a patient or experimental subject a reliable alteration in the expression pattern of at least one gene or a profile of genes correlated with incipient Alzheimer's disease (IAD) or Alzheimer's disease (AD) relative to expression of said profile or at least one gene in a pooled or individual control sample. The method comprises a) obtaining RNA from said body sample; b) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotide covalently attached to said array; and c) detecting the presence or absence of said alteration in the expression pattern of at least one gene correlated with incipient Alzheimer's disease (IAD) or Alzheimer's disease (AD) relative to expression of said at least one gene in a control. In preferred embodiments, the body sample may be a brain sample or neural tissue sample.

In a further aspect of the invention there is provided a method for diagnosing IAD in a patient. The method comprises a) obtaining a body sample from the patient and extracting RNA there

from; b) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotide covalently attached to said array; c) detecting the presence or absence of an alteration in the expression pattern of at least one gene correlated with incipient Alzheimer's disease (IAD) relative to expression of said at least one gene in a control; and d) using the presence of an alteration in the expression pattern of at least one gene correlated with incipient Alzheimer's disease (IAD) relative to expression of said at least one gene in a control to diagnose the presence of IAD. In another embodiment, the method further comprises administering MMSE or other neuropsychological test to the patient.

In yet a further aspect of the invention, there is provided a method of screening a test compound for treatment of AD or IAD. The method comprises a) administering the test compound to an animal or human exhibiting all or some of the symptoms of AD; b) obtaining a body sample from the animal and obtaining RNA there from; c) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotides covalently attached to said array; and c) detecting the presence or absence of an alteration in the expression pattern of at least one gene listed in Table 6 relative to expression of said gene in an untreated control animal or human exhibiting all or some of the symptoms of AD.

In another aspect of the invention there is provided a method of detecting an alteration in the expression pattern of a plurality of genes correlated with Alzheimer's disease relative to expression of said plurality of genes in a control in a brain tissue or neural tissue sample of an animal, said method comprising a) measuring the relative amount of individual proteins in said sample, wherein each of said proteins is encoded by a gene correlated with IAD; and b) correlating an increase or decrease in the amount of a plurality of said proteins relative to amount of said plurality of proteins to an alteration in the expression pattern of the plurality of genes

encoding said proteins. In preferred embodiments, the IAD associated genes are selected from those listed in Tables 6 or 4.

Brief Description of the Drawings

Figure 1 is a cartoon of a gene identification algorithm. (A) Genes rated absent were excluded from analysis. (B) Only annotated probe sets (not expressed sequence tags) were included in the statistical analysis. (C) Pearson correlation was performed for every gene against both MMSE and NFT measures of each subject. Venn diagram shows the number of genes significantly correlated ($P \leq 0.05$) with both MMSE and NFT or either index alone. For each index the false discovery rate (FDR) was calculated. (D) For the genes found to correlate significantly across all subjects (overall, $n=31$), another Pearson's correlation was performed post hoc among only the subjects rated "Control" or "Incipient" (Incipient, $n=16$).

Figure 2. Graphs of examples of correlated genes illustrating the four directions of correlation through which genes were identified. For each gene, expression density is plotted on the y axis, and MMSE (A left and C left) or NFT (B right and D right) scores are plotted on the x axis; R^2 value, P value (Pearson's test), linear fit (black line), and 95% confidence intervals (dashed lines) are also shown. (A and B) Genes for which expression levels were up-regulated with AD, identified with negative or positive correlation with MMSE (A) or NFT (B) scores, respectively. (C and D) Genes for which expression levels were down-regulated with AD, identified by negative or positive correlation with MMSE (C) or NFT (D), respectively. The MMSE scale is reversed, so that more advanced AD increases to the right on both indexes.

Figure 3. Table 5. A list of AD-correlated genes, probes and data showing correlation to AD, IAD, NFT, and/or MMSE. Alzheimer's disease genes (ADGs) are listed in alphabetical order by

gene name for up-regulated (positively correlated with NFT_0 and/or negatively correlated with $MMSE_0$) and down-regulated (negatively correlated with NFT_0 , and/or positively correlated with $MMSE_0$) categories. Description, gene title from Affymetrix annotation database. NFT_0 and $MMSE_0$, overall Pearson's correlations with neurofibrillary tangle (NFT-former) and Mini-Mental Status Exam (MMSE-latter) for all 31 subjects. NFT_1 and $MMSE_1$, correlations across only control and incipient subjects ($n = 16$). Negative correlations have negative P values. ANOVA, P value for one-way ANOVA tests across the following groups: control, incipient, moderate, and severe. Gene expression data for each group are mean \pm SEM

Figure 4. Table 6. A list of IAD-correlated genes, probes and data showing correlation to IAD. Incipient Alzheimer's disease genes (IADGs) are listed in alphabetical order by gene name for up-regulated (positively correlated with NFT_1 and/or negatively correlated with $MMSE_1$) and down-regulated (negatively correlated with NFT_1 , and/or positively correlated with $MMSE_1$) categories. Description, gene title from Affymetrix annotation database are provided. NFT_0 and $MMSE_0$, overall Pearson's correlations with neurofibrillary tangle (NFT-former) and Mini-Mental Status Exam (MMSE-latter) for all 31 subjects. NFT_1 and $MMSE_1$, correlations across only control and incipient subjects ($n = 16$). Negative correlations have negative P values. ANOVA, P value for one-way ANOVA tests across the following groups: control, incipient, moderate, and severe. Gene expression data for each group are mean \pm SEM.

Detailed Description of the Invention

The present inventors addressed the problems of high complexity and overlapping criteria for diagnosing incipient AD (IAD) by using a strategy that combines a powerful new gene microarray technology, which permits measurement of the expression of many thousands of genes simultaneously, with statistical correlation analysis. This strategy has allowed the linking

of gene expression to cognitive and pathological markers independent of AD diagnosis and has led to the identification of genes correlating with AD and in particular, IAD.

Several microarray studies of AD brain and/or mouse models of AD have been published. For example, US 6,838,592 discloses a mouse model for Alzheimer's disease, and US 6,852,497 discloses a transgenic mouse for testing compounds useful for AD. The microarray studies have yielded important new insights, in particular, regarding changes in plasticity-related genes (*e.g.*, Dickey *et al.*, (2003) *J. Neurosci.*, 23:5219-5226). However, few microarray studies use independent sample sizes to provide the statistical power needed to avoid high false positive (type I) and/or high false negative (type II) error (Miller *et al.*, (2001) *J. Gerontol. A Biol. Sci. Med. Sci.*, 56:B52-B57; Blalock *et al.*, (2003) *J. Neurosci.*, 23:3807-3819). In contrast to these applications, in the development of the present invention, adequate power was ensured by using a separate array for each hippocampal sample of a large group of subjects (n=31) and correlating the expression values of each of thousands of genes with pathological and cognitive indexes of incipient AD. The subjects in the AD study were assigned to four groups reflecting different levels of AD severity (incipient, moderate or severe) or control (Table 1), but the correlation analyses were independent of this initial diagnosis. Together, these approaches represent the first formal statistical correlation analysis between pathological markers of AD and thousands of genes on a microarray. The set of correlated genes therefore comprises a unique and valuable set of genes that, together or in small subsets, can be used to diagnose AD with greater accuracy than has been possible. Further, because these analyses revealed a major and previously unrecognized transcriptional response with important implications for the early pathogenesis of AD, these lists of correlated genes can be used to screen and develop new compounds for the treatment of AD.

Based on these large-scale studies, a list of genes that correlate with Alzheimer's disease (ADGs) that appear to have considerable potential importance for assessing AD and IAD and generating new treatments for AD has been generated (TABLES 5 and 6). These lists contain some genes, or proteins encoded by said genes, that were identified previously as being linked to AD (*e.g.*, inflammation-related genes) but none has been previously shown to be formally correlated with IAD. Further, many genes on the lists have not even been shown previously to be linked to AD or IAD. Thus, the lists of Alzheimer's disease-related genes (ADGs) or incipient-correlated ADGs (IADGs) are unique and useful biomarkers and therapeutic targets specifically for AD and/or IAD. In addition, the list of all genes whose expression pattern changes with IAD and/or AD contains many genes never before reported to change with AD or IAD, and therefore provides a useful and unique panel of gene biomarkers and therapeutic targets for study and treatment of AD.

Using the method of the invention, a number of processes and pathways that previously have not been clearly associated with AD have been identified. The present inventors have discovered that widespread changes in genomic regulation of multiple cellular pathways are major correlates of incipient AD and hence, further developed AD. As noted, it has been recognized previously that inflammation, synaptic dysfunction, energy failure, glial reactivity, protein misprocessing or misfolding, lipogenesis and cell cycle disturbances accompany AD. However, the main transcriptional orchestration seen in incipient AD may provide a new perspective on the possible origins of these deleterious processes, and provide new targets for therapy. In addition, the widespread activation of growth, differentiation, and tumor suppressor (TS) pathways, and the apparent collapse of protein-processing machinery so early in the disease, suggest clues to the early pathogenesis of AD. The detection of these process patterns also provides a diagnostic tool

for incipient AD and more progressive AD. These conclusions are supported by high levels of statistical confidence for individual genes and by statistical evidence of co-regulation of genes within related pathways and categories (Tables 2 and 3).

Multiple tumor suppressors (TSs), some of which regulate the cell cycle, were identified using the present method within the TF (Table 4) and other categories. Previous studies have found evidence of cell cycle reentry in neurons of the AD brain (Arendt *et al.*, (2000) Ann. N.Y. Acad. Sci., 920:249-255; Bowser *et al.* (2002) J. Alzheimer's Dis. 4:249-254), and a handful of studies have also examined TSs in relation to AD, largely in terms of their roles in apoptotic pathways (e.g., p52) (See Bowser *et al.*, supra). However, TSs have other actions unrelated to apoptosis and can, in fact, be antiapoptotic (See Slack *et al.* (1995) J. Cell Biol., 129:779-788). Notably, TSs play critical roles in cellular differentiation related to development and tumor suppression. For example, overexpression of some TSs (e.g., RB proteins) induces cell cycle arrest, differentiation, and process extension in astrocytomas (See Galderisi *et al.* (Mol. Cell. Neurosci., 17:415-425). TS expression also is necessary for neurite extension and synaptogenesis in neuronal development (See Slack *et al.*, supra). Moreover, in some cell types, TSs operate by inducing cellular senescence and inhibiting protein biosynthesis (Campisi, J. (2001) Trends Cell Biol., 11:S27-S31).

TSs can be activated by developmental factors, DNA/cellular damage, or dysregulation of the cell cycle. Therefore, oxidative stress, inflammation, or abnormal CA^{2+} signaling are clearly candidate activators of TSs. In addition, TSs act as negative feedback regulators of growth and are often elevated in response to excess growth factor (GF) production in tumors (73). Many unregulated DGs also were identified here (Table 4), perhaps originating in OGs and their progenitors, which retain substantial growth potential in adult brain. Consistent with this

possibility, several of the up regulated IADGs, including PDGFB, FYN, and FGFR3, play major roles in OG proliferation, differentiation, and myelinogenesis.

The present studies have revealed widespread and apparently orchestrated transcriptional responses associated with early signs of AD pathology. Dissecting the bases for these early responses should yield important insights into pathogenic mechanisms and suggest therapeutic approaches to AD. Further, by testing for changes in the pattern of gene expression of the genes shown herein to be correlated with AD or IAD, or subsets of these genes, an accurate diagnosis of AD or IAD can be made. Gene expression patterns for these genes, and/or subsets thereof, may be determined by microarray assay or any convenient screening method that enables simultaneous screening of several genes listed in Tables 4, 5 and/or 6, *e.g.*, ten different AD-correlated genes, to several thousand AD-correlated genes, *e.g.*, all of the genes listed in Table 5 or 6. For example, a diagnostic assay for AD or IAD may include screening for either up-regulation or down-regulation (as appropriate) of a subset of the genes listed in Table 5, such as for example, the genes listed in Table 6, or a smaller subset of the listed genes. Detection of a change in expression of a statistically significant percentage of genes shown herein to be correlated with IAD or AD is indicative that the patient has IAD or AD.

A subset of ADG or IADGs specifically linked to a process or system identified in Table 2, 3 or both (*e.g.*, regulation of transcription, cell proliferation, oncogenesis, *etc.*), may be used in a microarray to test efficacy of a new compound targeted to slowing or reversing AD, either in experimental tests to develop new compounds, or as diagnostic or therapeutic guides. Similarly, such a subset of genes may be used in an assay, *e.g.*, microarray-based assay, as a diagnostic tool for IAD or AD.

In a preferred embodiment an assay for changes in the pattern of expression of genes shown to be correlated with AD or IAD, such as a microarray-based assay, includes probing for expression of genes categorized as transcription factors (TFs). For example, a screen for AD or IAD may include probes for those genes listed in Table 4, or a subset of the genes in Table 4, such as the genes demarcated with an asterisk, the genes in boldface, the underlined genes, or combinations thereof.

The assay for probing expression of genes correlated with AD and/or IAD can be an RNA-based microarray for example. Changes in the pattern of gene expression of many genes can be identified simultaneously by hybridizing a control RNA sample and a sample of RNA obtained from a sample from a patient, such as for example a neural tissue sample, or brain biopsy to high density arrays containing several (*e.g.*, five to ten or more), hundreds or thousands of oligonucleotide probes correlating to the genes or subsets of the genes identified herein as genes correlating to AD or IAD (Tables 5 and 6) (Cronin et al., (1996) Human Mutation 7:244-255; Kozal et al., (1996) Nature Medicine 2:753-759). The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 or 12 nucleotides to about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20 to 25 nucleotides, which can be used in PCR amplification or a hybridization assay, or a microarray. As used herein, oligonucleotide is substantially equivalent to the term "probe", as commonly defined in the art. An oligonucleotide can be a cDNA sequence.

Hybridization conditions for detecting alterations in the expression pattern of ADGs or IADGs are readily determined by those of skill in the art. In general, high stringency hybridization conditions are used.

The terms "stringent conditions" or "stringency", as used herein, refer to the conditions for

hybridization as defined by the nucleic acid, salt, and temperature. These conditions are well known in the art and may be altered in order to identify or detect identical or related polynucleotide sequences. Numerous equivalent conditions comprising either low or high stringency depend on factors such as the length and nature of the sequence (DNA, RNA, base composition), nature of the target (DNA, RNA, base composition), milieu (in solution or immobilized on a solid substrate), concentration of salts and other components (e.g., formamide, dextran sulfate and/or polyethylene glycol), and temperature of the reactions (within a range from about 5° C below the melting temperature of the probe to about 20° C to 25° C below the melting temperature). One or more factors may be varied to generate conditions of either low or high stringency different from, but equivalent to, the above listed conditions.

Alternatively, the assay for detecting changes in expression patterns of ADGs and/or IADGs may be a protein- or an antibody-based assay in which the probes (antibodies) are specific for proteins encoded by the genes or a subset of the genes listed in Table 6. The test sample for an antibody-based assay, such as a microarray, Western blot analysis, ELISA screening, etc., would comprise screening proteins encoded by genes correlated with IAD or AD which are obtained from a body sample, such as spinal fluid, neural tissue or brain tissue, for an alteration in the amount of a plurality of proteins relative to the amount of the proteins in a control sample obtained from a non-AD individual or a pooled non-Ad sample. The sequences of the genes, and hence, the proteins encoded by the genes listed in Tables 4, 5 and 6 are known and publicly available, and are incorporated herein. Also, the person of ordinary skill in the art can use knowledge of the published sequences to generate appropriate probes for screening those genes of interest or may purchase commercially available probes for the genes of interest.

An alteration in the expression pattern of a statistically significant number of genes is indicative of a diagnosis of AD or IAD. Confirmation of a diagnosis of AD or IAD on the basis of an overall change in the pattern of gene expression of the tested genes correlated with AD or IAD may be made by MMSE for example, or other neurological test or test used to ascertain cognitive ability.

The details of one or more embodiments of the invention are set forth in the accompanying description above. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. Other features, objects, and advantages of the invention will be apparent from the description and from the claims. In the specification and the appended claims, the singular forms include plural referents unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All patents and publications cited in this specification are incorporated by reference.

The following Examples are presented in order to more fully illustrate the preferred embodiments of the invention. These examples should in no way be construed as limiting the scope of the invention, as defined by the appended claims.

Example 1.

Human Brain Samples and Pathologic/Cognitive Assessment. Hippocampal specimens used in this study were obtained at autopsy from 35 subjects (16 female and 19 male; Table I) through the Brain Bank of the Alzheimer's Disease Research Center at the University of Kentucky. At autopsy, coronal sections of the left hippocampus (3-5 mm) were immediately frozen in liquid nitrogen and

stored at -80°C until analyzed. Adjacent sections were fixed in 10% formalin and used for neuropathologic evaluation. Except for borderline AD subjects (see below), all AD patients met Alzheimer's Disease and Related Disorders Association criteria for the clinical diagnosis of AD and Consortium to Establish a Registry for Alzheimer's Disease and National Institute of Aging-Reagan Institute neuropathology criteria for the diagnosis of AD. The frozen hippocampal tissues were warmed to -20°C to enable dissection of CA1 and CA3 under a Zeiss surgical microscope.

Table 1.

	Control (n=9)	Incipient (n=7)	Moderate (n=8)	Severe (n=7+)
Age	85.3±2.7	90±2.1	83.4±1.1	84±4.0
NFT	2.7±1.0	9.4±1.8	25.6±3.5	32.7±7.2
Braak	2.1±0.4	5±0.4	5.6±0.2	5.9±0.1
NMSE	27.7±0.5	24.3±1.1	16.5±0.6	6±1.4
PMI	2.6±0.2	3.3±0.6	3.2±0.2	3±0.1

Values are mean ± SEM. PMI= postmortem interval.

The MiniMental State Examination (MMSE) is a reliable index of AD-related cognitive status at a given point in time (Clark *et al.* (1999) Arch. Neurol., 56:857-862). However, its rate of decline varies with severity, and mildly impaired patients show little MMSE decline even after several years (Clark *et al.*, supra). Recent MMSE data were available for most subjects but, in subjects for whom the interval between the most recent MMSE score and death was >1 year, the MMSE score was adjusted downward by one point per year. This approach likely

underestimates MMSE decline for severely affected patients but seemed suitable for this study, given the slow MMSE decline in less impaired subjects (Clark *et al.*, supra) and the focus on such subjects. Postmortem scores on AD-related pathologic indices for Braak staging, hippocampal neurofibrillary tangles (NFT), and diffuse and neuritic senile plaques were determined as described (Geddes *et al.* (1997) *Neurobiol. Aging*, 18:S99-S105). The MMSE and NFT values were selected as primary markers for quantifying AD progression because of the Braak scale's limited range and because the observed NFT results correlated more closely with the MMSE ($r = 0.45$) than did the observed plaque values ($r = 0.19$), consistent with prior findings (See Hyman, B.T. (1997) *Neurobiol. Aging*, 18:S27-S32). Further, the evidence that soluble rather than deposited Beta Amyloid may be more relevant to cognitive impairment is mounting (Klein *et al.* (2001) *Trends Neurosci.*, 24:219-224; Price *et al.* (1998) *Annu. Rev. Neurosci.*, 21:479-505; Morgan, D. (2003) *Neurochem.*, 28:1029-1038).

Based primarily on MMSE criteria (Mitchell, *et al.*, *Ann. Neurol.*, 51:182-189; Clark *et al.*, supra), subjects were categorized initially into four groups, termed "Control" (MMSE >25), "Incipient AD" (MMSE 20-26), "Moderate AD" (MMSE 14-19), and "Severe AD" (MMSE <14) (Table I). Several borderline cases (e.g., MMSE = 26) were assigned based on NFT, amyloid plaque, and Braak stage data. In addition, four subjects exhibited more cognitive deterioration (MMSE <20) than expected from their NFT or amyloid scores. Because these subjects were potentially affected by confounding conditions, they were excluded from the analyses, leaving $n = 31$ overall.

RNA Isolation and Affymetrix GeneChip Processing. Procedures for total RNA isolation, labeling, and microarray processing were similar to those described (Blalock *et al.*, supra), except that human GeneChips (HG-U133A) and MICROARRAY SUITE 5 (MAS5; Affymetrix,

(2001) Affymetrix Microarray Suite User's Guide (Affymetrix, Santa Clara, CA, version 5) were used. Each subject's CA1 subfield RNA was processed and run on a separate chip. An average yield of 55 µg of biotin-labeled cRNA target was obtained from 8 µg of total RNA each per CA1 sample, of which 20 µg of cRNA was applied to one array. cRNA yield did not differ significantly among groups ($P = 0.32$), but the most severe AD group exhibited a trend toward lower cRNA levels, possibly reflecting greater cellular degeneration.

Microarray Data Analysis. Scaling and noise analyses were performed as described (Blalock *et al. supra*) and Affymetrix algorithms for signal intensity and presence P values (Affymetrix, *supra*), respectively, were used to determine expression (relative abundance) and detection reliability of transcripts. A gene probe set was rated "present" if it was detected on at least four chips in the study. Individual values were blanked and treated as missing values if they were >2 SD away from the group mean. Finally, probe sets were considered "genes" if they had been assigned a "gene symbol" annotation (Affymetrix database). Pearson's correlation tests and ANOVAs were performed in EXCEL 9.0 data copied from the MASS pivot table, as described (Blalock *et al. supra*).

Biological Process Categorization by Gene Ontology. As noted, microarray studies face substantial false-positive concerns because of the large multiple comparison error. Conversely, however, they can also strengthen statistical confidence by providing evidence of coregulation of multiple genes that are related by function of pathway (See Ashburner *et al.*, (2000) Nat. Genet., 25:25-29). In the present study, a new software tool, the EXPRESSION ANALYSIS SYSTEMATIC EXPLORER (EASE)(available from NIAID), to assign identified genes to "GO: Biological Process" categories of the Gene Ontology Consortium (Ashburner *et al.*, *supra*) and to test statistically (EASE Score, a modified Fisher's exact test) for significant coregulation (overrepresentation) of identified genes within each biological process category.

Gene Identification Algorithm (Fig. 1). To test thousands of genes for correlation with AD markers, while still managing multiple comparison error, all "absent" or undefined (expressed sequence tags) genes (Fig. 1 A and B) were excluded, thereby reducing expected false positives. Pearson's test was then used to test each of the 9,921 remaining genes for its correlation with MMSE and NFT scores (Fig. 1C). A total of 3,413 genes were significantly associated (at P values of ≤ 0.05) with the MMSE, NET, or both, across all 31 subjects (overall correlations). These correlated genes were termed "AD-related genes" (ADGs).

For both the MMSE and NFT analyses, the false discovery rate, *i.e.*, number of false positives expected because of multiple comparisons divided by the total positives found, was calculated. The false discovery rate provides a worst-case probability that any gene identified (e.g., at $P < 0.05$) by correlation is significant because of the error from multiple testing. The observed false discovery rates (~ 0.20 ; Fig. 1) are reasonably low for a microarray study, in particular, considering the relatively relaxed P value ($P \leq 0.05$), indicating good statistical power. (The false discovery rate generally decreases with more stringent P value criteria. However, the confidence lost with a relaxed P value is substantially offset by the increased confidence gained from expanding the overall number of identified genes and strengthening the EASE analysis of co-regulation).

Because NFT scores increase and MMSE scores decrease with AD severity, genes up-regulated with AD could only correlate positively with NFT scores and negatively with the MMSE, whereas genes down-regulated with AD could only correlate positively with the MMSE and negatively with NFT scores. Fig. 2 illustrates examples of the four patterns of correlation that were possible for ADCs. Overall, 1,977 ADCs were up-regulated and 1,436 were down-

regulated. More were correlated with the MMSE than with NET scores. The full set of all identified ADCs is included in Table 5, which is published as supporting information on the PNAS web site.

In a subsequent step (Fig. ID), those genes within this large set of ADGs that also correlated with AD markers across a smaller subgroup comprising incipient AD and control subjects (i.e., all subjects with MMSE ≥ 20 and NFT < 20) ($n = 16$) were identified post hoc. Within this subset, only genes correlated in the same direction as their overall correlations were considered. Of the 3,413 overall ADGs, 609 were found also to correlate significantly (at P values of ≤ 0.05) in the incipient subgroup, 258 with the MMSE, 262 with NFT scores, and 89 with both (termed "Incipient ADCs" or IADGs). More IADGs were up-regulated with AD (431 genes) than were down-regulated (178 genes) (see Table 6, which is published as supporting information on the PNAS web site, for alphabetical lists of all IADGs).

Biological Processes Associated with ADGs and IADGs. Using EASE analysis, biological process categories that showed a disproportionately high number of co-regulated genes (significant overrepresentation of ADGs or IADGs in those categories) were identified. The Gene Ontology Biological Process categories in which ADGs were overrepresented by EASE score (in general, at P values of ≤ 0.05) are shown in Table 2. The overrepresented categories for IADGs are shown in Table 3. Because of the reduced number of genes and lower statistical power in this post hoc analysis, however, the significance level for identified categories of IADGs was set at $P \leq 0.15$.

Tables 2 and 3 list significant functional categories having a higher ratio of identified genes to all genes tested on an array for association with that category, relative to the ratio of total identified

genes in the study to all genes tested on the array for associations with all categories.

Association numbers approximate but are not exactly equal to gene numbers in a category. After each category description (in parentheses) is the ratio of associations for that category and the percentage represented by that ratio. The analogous ratios for total identified up-regulated and down-regulated genes are shown in the headings (Total). EASE, modified Fisher's exact test P value; N/M/B, percentage of genes included in category because they were significant by NFT correlation (N), NMSE correlation (M), or both (B). The complete list of identified ADGs is given alphabetically in Table 5.

Table 2. Biological process categories overrepresented by IADGs

Up-regulated (Total: 1,572/6,265; 25.1%)	EASE	N/M/B	Down-regulated (1,126/6,265; 18.0%)	EASE	N/M/B
Regulation of transcription (269/792; 34%)	0.0000	21/38/41	Energy pathways (17/151; 37.7%)	0.0000	15/15/69
Cell proliferation (210/666; 31.5%)	0.0001	23/43/35	ATP biosynthesis (16/23; 69.6%)	0.0000	18/9/73
Oncogenesis (24/47; 51.1%)	0.0003	21/39/39	Synaptic transmission (49/143; 34.3%)	0.0000	9/30/61
Protein amino acid phosphorylation (104/310; 33.5%)	0.0006	23/30/47	Coenzyme biosynthesis (20/40; 50%)	0.0000	15/15/69
Transition metal ion homeostasis (10/16; 62.5%)	0.0076	18/45/36	Cation transport (60/197; 30.5%)	0.0000	13/18/69
Positive regulation cell proliferation (25/62; 40.3%)	0.0119	18/68/14	Protein folding (30/86; 34.9%)	0.0003	32/11/57
Chromatic architecture (34/94; 36.2%)	0.0186	25/43/33	Tricarboxylic acid cycle (12/222; 54.5)	0.0006	27/27/47
Nucleosome assembly (13/27; 48.1%)	0.0219	11/56/33	Glycolysis (14/29; 48.3%)	0.0007	6/18/76
Histogenesis and organogenesis (22/57; 38.6%)	0.0319	22/17/61	Neurogenesis (64/244; 26.2%)	0.0011	19/27/53
Cell adhesion 0.0425(94/314; 29.9%0.)	0.0346	19/46/35	Amino acid catabolism (13/30; 43.3%)	0.0038	33/0/67
Development (235/850; 27.6%)	0.0425	21/42/37	Ubiquitin-dependent protein catabolism (27/87; 31%)	0.0043	48/13/39
Complement activation, classical (9/18; 50%)	0.0576	10/40/50	Secretion (14/37; 37.8%)	0.0095	03/35/65
Negative regulation cell proliferation (28/83; 33.7%)	0.0762	09/50/41	Protein transport (66/288; 22.9%)	0.0245	26/25/49
Isoprenoid metabolism (6/10; 60%)	0.0789	00/83/17	Neurotransmitter metabolism (6/11; 54.5%)	0.0329	17/17/67
Apoptosis (72/255; 29.5%)	0.0818	13/32/55	Axon guidance 8/19; 42.1%)	0.0404	27/9/64

Defense response (102/360; 28.3%)	0.1010	15/57/28	Calcium ion transport (11/32; 34.4%)	0.0482	7/7/87
Lipid metabolism (82/288; 28.5%)	0.1250	15/47/38	Microtubule-based process (20/73; 27.4%)	0.0538	11/21/68

Biological process categories significantly overrepresented by ADGs ($P \leq 0.05$; EASE SCORE) and a few other selected categories are shown. Numerous other similar significant categories are not included to reduce redundancy. Significant functional categories are those with a higher ratio of identified genes to all genes tested on the array for associations with that category, relative to the ratio of total identified genes in the study to all genes tested on the array for associations with all categories. Association numbers approximate but are not exactly equal to gene numbers in a category. After each category description (in parentheses) is the ratio of associations for that category and the percentage represented by that ratio. The analogous ratios for total identified up-regulated and down-regulated genes are shown in the headings (Total). EASE, modified Fisher's exact test P value; N/M/B, percentage of genes included in category because they were significant by NFT correlation (N), MMSE correlation (M), or both (B). (The complete list of ADGs is given alphabetically in Table 5).

Table 3. Biological process categories overrepresented by incipient correlations (IADGs)

Up-regulated (Total: 379/6,265; 6%)	EASE	N/M/B	Down-regulated (154/6,265; 3%)	EASE	N/M/B
Regulation of transcription, DNA... (64/7881; 8%)	0.008	30/49/21	Protein folding (13/86; 15%)	0.000	71/21/7
Histogenesis and organogenesis (9/57; 16%)	0.020	33/44/22	Axon cargo transport (3/5; 60%)	0.006	67/33/0
Chromatin assembly/disassembly (8/52; 15%)	0.035	22/78/0	Synaptic transmission (10/143; 7%)	0.008	33/67/11
Cell proliferation (52/666; 8%)	0.041	30/46/23	Protein metabolism (46/1,415; 3%)	0.028	64/28/9
Cell adhesion (26/314; 8%)	0.092	36/46/18	Microtubule-based movement (4/33; 12%)	0.046	50/50/0
Development (61/850; 7%)	0.103	38/43/19	Electron transport (10/200; 5%)	0.055	45/36/18
Protein amino acid phosphorylation (25/310; 8%)	0.122	38/46/15	Cytokinesis (5/61; 8%)	0.061	60/20/20
Cell motility (18/182; 9%)	0.134	35/41/24	Intracellular transport (15/369; 4%)	0.066	58/37/5
Lipid metabolism (23/288; 8%)	0.148	48/39/13	GPCR signaling pathway (11/264; 4%)	0.111	33/53/13
Apoptosis (20/244; 8%)	0.150	24/62/14	Cell surface signal transduction (17/492; 4%)	0.145	43/48/10

Biological process categories significantly overrepresented by IADGs ($P \leq 0.15$; EASE SCORE) and a few other selected categories are shown. Numerous other similar significant categories are not included to reduce redundancy. Significant functional categories are those with a higher ratio of identified genes to all genes tested on the array for associations with that category, relative to the ratio of total identified genes in the study to all genes tested on the array for associations with all categories. The association numbers approximate but are not exactly equal to gene numbers in a category. After each category description (in parentheses) is the ratio of associations for that category and the percentage represented by that ratio. The analogous ratios for total identified up-regulated and down-regulated genes are shown in the headings (Total). EASE, modified Fisher's exact test P value; N/M/B, percentage of genes included in category because they were significant by NFT correlation (N), MMSE correlation (M), or both (B). (The complete list of IADGs is given alphabetically in Table 6).

Although many overrepresented categories were similar between Tables 2 and 3, notable differences also occurred. The categories shown in Table 3 were of particular interest because they reflect groups of genes correlated with AD markers in the incipient subjects. Transcription factor, proliferation, and development processes were among the largest categories of up-regulated IADGs. In addition, extracellular matrix/cell adhesion/motility processes, comprising multiple laminins (A2,4), integrins (A1,6,7), tenascins, collagens, cadherins, proteoglycans, and amyloid precursor protein were up-regulated. Of note, several individual members of the semaphorin/plexin pathway, which inhibits axonal elongation, also were up-regulated ADGs (e.g., SEMA3B and plexin 132) (Table 6). Further, histogenesis, apoptosis, phosphorylation, and

lipid metabolism, including prostaglandin synthesis, were overrepresented by up-regulated IADGs (Table 3). Although their categories were not overrepresented, several up-regulated IADGs reflected inflammatory and oxidative stress processes (e.g., IFN-gamma, IL-18, interleukin receptors, and AOP2) (Table 6).

For down-regulated categories, a major difference was seen between ADGs and IADGs, in that multiple protein metabolism categories, including folding and transport (immunophilins, chaperones, and heat shock proteins), were overrepresented by IADGs (Table 3), but not ADGs (Table 2). One of the hallmarks of AD, reduced energy metabolism, which dominated the down-regulated categories of ADGs (Table 2), was only reflected in one category, electron transport, of down-regulated IADGs (Table 3).

Calcium Signaling Regulation. Altered Ca^{2+} signaling is suspected of a role in AD and brain aging and also was identified in a recent microarray study of aging (Blalock *et al.*, supra). Although signaling pathways in general, including Ca^{2+} pathways and transport systems, were down-regulated in AD (Tables 2 and 3), some individual up-regulated Ca^{2+} -dependent IADGs included the CAMP response element-binding protein (CREB) cofactor (EP300), a calpain inhibitor (calpastatin), S100A4, and the Ca^{2+} -dependent death-associated protein kinase (DAPK2) (Table 6).

Transcription Factors (TFs). The TF category was the most significantly overrepresented by up-regulated IADGs and ADGs. Table 4 shows the TF-category IADGs correlated with NFT, MMSE scores, or both (only those correlated at P values of ≤ 0.025 are shown). Review of the functions of the identified TFs revealed that a disproportionately high number are tumor suppressors (TSs) or TS cofactors (boldface), including several of the retinoblastoma (RB)

family (also see Table 6 for additional RB members). Many other identified TFs are related to lipid/cholesterol biosynthesis and adipocyte differentiation (underlined). Numerous zinc finger TFs favoring transcriptional repression also were identified. Paradoxically, however, a considerable number of the remaining TFs are associated with growth or proliferation. In general, more up-regulated TFs for TS and lipogenesis were correlated with NFT scores than with MMSE, whereas more growth-related TFs were correlated with MMSE (Table 4; see Table 6 for gene descriptions).

Table 4. Up-regulated IADGs categorized as TFs

ANF253	<u>CEBPA</u>	+NFT	THG-1	KLF2
<u>SREBF1</u>	<u>NF1-C</u>	RBAK	ZNF268	RBL1(p107)*
CS0orf104	RBBP1	PML	ZBRK1	<u>PPARBP*</u>
<u>RXRB</u>	CERD4	GL12	GTF21	
		ASCL1		
		-MMSE		
SMARCC2	RUNX2	ZNF198	SP18	SP3
BRD1	TX1	CHD2	HMGB3	ENSR1
ANF32	LOC51580	HOXB5	HOXC4	Rpo1-2
ZNF7	C22orf	<u>NCOA3</u>	TCF3	PRKR
ZNF43	ID4	EP300	PB1	ZNF136*
ZNF254	ZNF237	ZNF83	ZNF84	

Gene symbols for TF IADGs positively correlated with NFT, negatively correlated with MMSE, or both (*) are shown separately (only those with $P \leq 0.025$). IADGs for TS (boldface) or lipogenic (underlined) functions are high-lighted. (Full descriptions of all IADGs, alphabetically listed, are available in Table 6).

*TF category IADGs correlated with both NFT and MMSE scores.

Tumor Suppressors (TS). The high proportion of TS-related TFs prompted us to inspect other biological process categories for genes with TS functions. Many IADGs with TS or cellular differentiation functions were found in the phosphorylation, apoptotic, cell cycle, and other categories (e.g., TGF- β , GSK3B, PDCD4, FZR1, SFRP1, AIM1, DAPK2, and CDK2AP1). Conversely, inspection of the down-regulated TF categories (not shown) revealed many TFs important for growth and proliferation, including several of the MYC family (MGA and IRLB)

and DPI(TFDP1), a member of the growth-promoting E2F family targeted by the RB family of TSs (Table 6).

PKA Pathways. The cAMP-dependent protein kinase (PKA) pathway stimulates growth in some cell types and differentiation and inhibition of growth in others. Several PKA-related genes were up-regulated IADGs, including A kinase-anchoring molecules (AKAP9, AKAP13, and CAP350), adenylate cyclase 7, and the PKA Type RII α regulatory subunit (Table 6).

Example 2.

Diagnosis of AD or IAD in a patient.

Total RNA is isolated from a neural tissue sample or tissue sample obtained from the patient using the TRIzol reagent and following the manufacturer's RNA isolation protocol (Invitrogen, #15596). For tissue samples, *e.g.*, brain tissue, one milliliter of TRIzol solution is added to each tube containing the frozen tissue block, and the tissue is homogenized by ten passages through an 18.5 gauge syringe needle. After centrifugation, the RNA is precipitated from the aqueous layer, washed, and dissolved in RNase-free water. RNA concentration and integrity are assessed by spectrophotometry and gel electrophoresis. The RNA samples may be stored at -80°C until use. Gene expression analyses are performed using the Affymetrix GeneChip System. Gene chips can be custom made to contain oligonucleotides specific to only a subset of human genes, such as those AD/IAD correlated genes listed in Table 5, or Table 6, or subsets of these genes. Subsets of these genes include genes identified in general in Tables 2, 3, and specifically in 4, and may comprise any combination of the genes identified in these tables. The gene chips may be made in any format to accommodate content requirements, ranging from 520 to over 61,000

sequences per array. Duplicates of the oligonucleotide sequences may be run on the same or on separate arrays as controls.

The labeling of RNA samples, GeneChip (HG-U133A) hybridization, and array scanning are performed according to the Affymetrix GeneChip Expression Analysis Manual (Version 5, (2000)). For brain tissue, each CA1 subfield RNA is processed and run on a separate gene chip. For other tissue samples duplicate chips may be made and tested. Briefly, about 20 µg of cRNA is applied to one chip. The hybridization is run overnight in a rotating oven at about 45°C. The chips are then washed and stained on a fluidics station and scanned at a resolution of about 3 µm in a confocal scanner (*e.g.*, Agilent Affymetrix GeneArray Scanner).

Microarray suite software (MAS 5.0, Affymetrix) is used to calculate the overall noise of the image (Qraw).

The algorithms used to determine average difference expression (ADE) scores (expression level) and presence/absence calls are described in the Microarray Suite 5.0 Manual and form the basis for determining expression (relative abundance) of transcripts and whether a particular transcript is reliably detectable, respectively.

Example 3

Drug Screening

Compounds are tested as potential therapeutic agents for AD by administering a test compound to an animal exhibiting all or some of the symptoms of AD. Various animal models can be used to analyze effects of test compounds on the expression of ADGs and/or IADGs, as described above. Preferred are animals such as mice that exhibit characteristics associated with the pathophysiology of AD. Administration of the test compound in a pharmaceutically effective carrier and *via* an administrative route that reaches the target tissue in an appropriate therapeutic

amount is preferred.

Analysis of ADG and /or IADG expression in the brain tissue of the mice after exposure to the test compound in comparison to expression observed in control animals is a preferred method of determining the effect of the test compound on genes and/or biological pathways associated with AD.

What is claimed:

1. An oligonucleotide array comprising a solid support comprising a plurality of different oligonucleotide probes, each oligonucleotide probe specific for a gene listed in Table 6.
2. The oligonucleotide array according to claim 1 wherein each oligonucleotide probe is specific for a gene listed in Table 4.
3. The oligonucleotide array of claim 1 wherein said plurality of oligonucleotide probes comprises probes for genes encoding human transcription factors, proliferation-associated protein, tumor suppressor proteins, histogenesis-associated protein, apoptosis-associated protein, phosphorylation enzymes, lipid metabolism-associated proteins, extracellular matrix, cell adhesion protein, motility protein, laminin, integrin, tenascin, collagen, cadherin, proteoglycan, SEM3AB, plexin B2, and combinations thereof.
4. A method of detecting in a brain tissue or neural tissue sample an alteration in the expression pattern of a plurality of genes correlated with incipient Alzheimer's disease (IAD) relative to expression of said plurality of genes in a control comprising
 - a) obtaining RNA from said sample;
 - b) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotides covalently attached to said array; and
 - c) detecting the presence or absence of said alteration in the expression pattern of said plurality of genes correlated with IAD relative to expression of said plurality of genes in a control.
5. The method according to claim 4 wherein the sample is a brain sample.

6. The method of claim 4 wherein the sample is a neural tissue sample.
7. The method of claim 4 wherein the array comprises oligonucleotides selected from the group of probes listed in Table 4.
8. A method for diagnosing AD in a patient comprising
 - a) obtaining a brain tissue or neural tissue sample from the patient and extracting RNA therefrom;
 - b) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotides covalently attached to said array;
 - c) detecting the presence or absence of an alteration in the expression pattern of a plurality of genes correlated with incipient Alzheimer's disease (IAD) relative to expression of said plurality of genes in a control; and
 - d) correlating the presence of an alteration in the expression pattern of said plurality of genes correlated with IAD relative to expression of said plurality of genes in a control to the presence of AD.
9. The method of claim 8 further comprising administering a mini mental state examination (MMSE) or neurological test for AD or IAD to the patient and correlating the results with the presence or absence of AD.
10. The method of claim 8 wherein the sample is a brain sample.
11. The method of claim 8 wherein the sample is a neural tissue sample.

12. The method of claim 8 wherein the array comprises oligonucleotide probes selected from the group of probes listed in Table 4.

13. A method of screening a test compound for treatment of AD or IAD comprising,

a) administering the test compound to an animal or human exhibiting all or some of the symptoms of AD;

b) obtaining a brain tissue or neural tissue sample from the animal or human and obtaining RNA there from;

c) contacting said RNA with an array according to claim 1 under conditions that permit hybridization of said RNA to oligonucleotide probes covalently attached to said array; and

d) detecting the presence or absence of an alteration in the expression pattern of a plurality of genes correlated with IAD relative to expression of said plurality of genes in an untreated control animal or human exhibiting all or some of the symptoms of AD.

14. A kit comprising an array according to claim 1 and at least one reagent .

15. The kit according to claim 14 wherein the array comprises oligonucleotide probes selected from the group of probes listed in Table 4.

16. A method of detecting an alteration in the expression pattern of a plurality of proteins encoded by genes correlated with incipient Alzheimer's disease (IAD) relative to expression of said plurality of proteins in a control in a brain tissue, neural tissue or spinal fluid sample of an animal, said method comprising

- a) measuring the relative amount of individual proteins in said sample, wherein each of said proteins is encoded by a gene correlated with IAD; and
- b) correlating an increase or decrease in the amount of a plurality of said proteins relative to amount of said plurality of proteins to an alteration in the expression pattern of the plurality of genes encoding said proteins.

17. The method of claim 16 wherein the plurality of genes is selected from the group of genes listed in Table 6.

18. The method of claim 16 wherein the plurality of genes is selected from the group of genes listed in Table 4.

19. A method for diagnosing AD in a patient comprising

- a) obtaining a brain tissue, neural tissue or spinal fluid sample from the patient and extracting protein there from;
- b) measuring the relative amount of individual proteins in said sample, wherein each of said proteins is encoded by a gene correlated with IAD; and
- c) correlating an increase or decrease in the amount of a plurality of said proteins relative to amount of said plurality of proteins to the presence of AD in said patient.

20. The method of claim 19 wherein each of the plurality of proteins is encoded by a gene listed in Table 6.

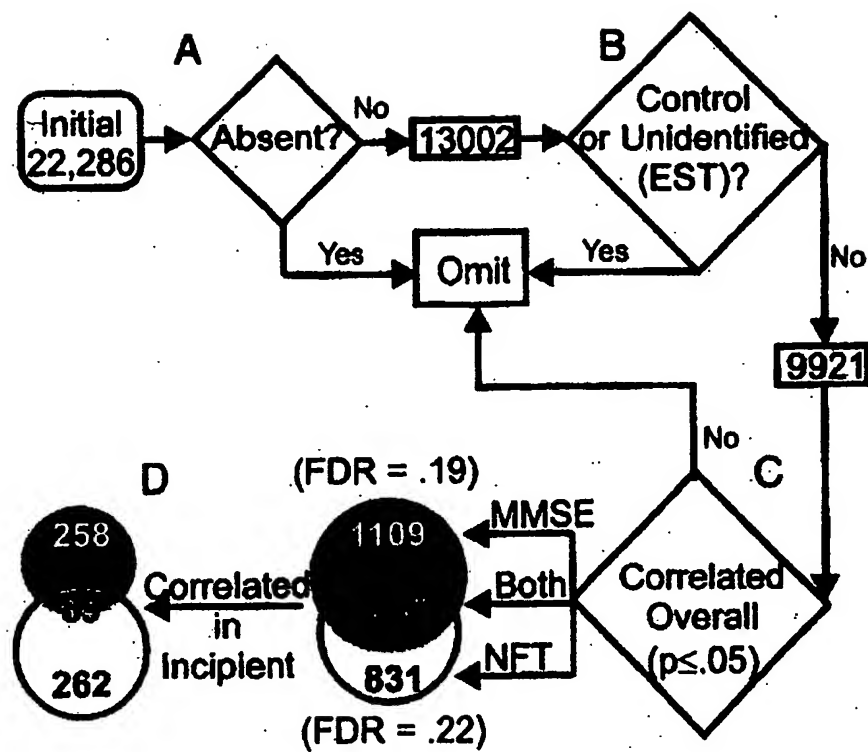


FIGURE 1

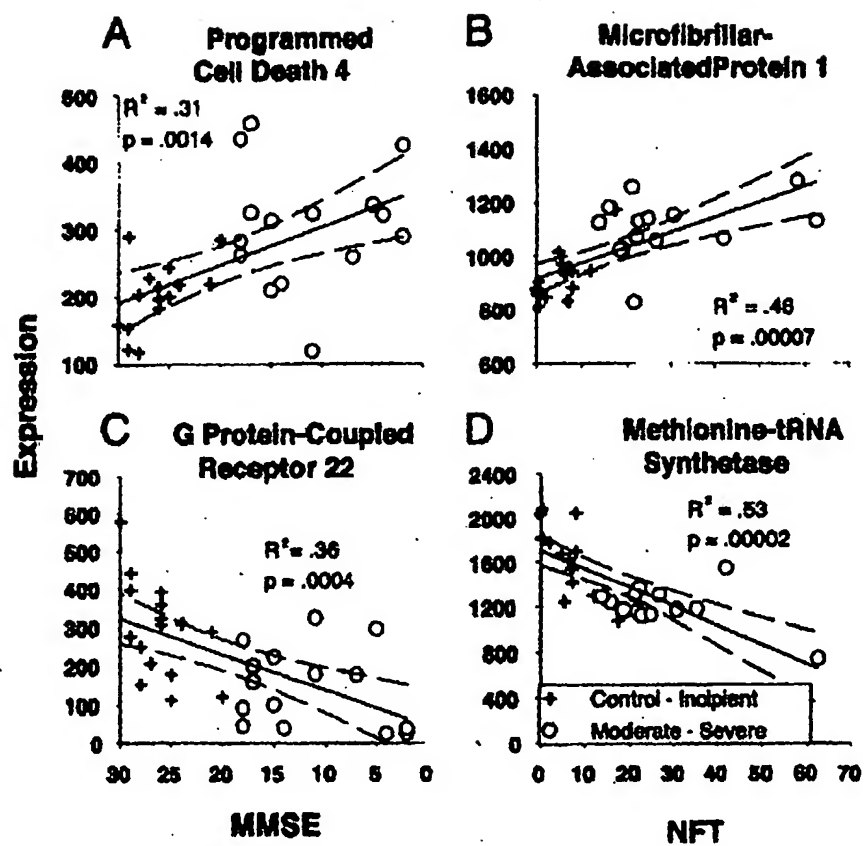


FIGURE 2

Upregulated

Probe set Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
205056_s_at	protein "A"	0.0410	-0.3550	0.4930	0.0523	0.4430	430 ± 38	443 ± 116	493 ± 21	563 ± 41
205986_at	apoptosis-associated tyrosine kinase	0.0229	-0.0469	0.0979	-0.3946	0.0212	2012 ± 85	2454 ± 180	1958 ± 129	3320 ± 611
204177_s_at	Kelch motif containing protein	0.0017	-0.0012	0.0959	-0.0389	0.0023	344 ± 23	396 ± 11	498 ± 32	504 ± 50
203505_at	ATP-binding cassette, sub-family A, member 1	0.0009	-0.0024	0.0432	-0.2938	0.0084	802 ± 124	1093 ± 209	1153 ± 127	2307 ± 574
212772_s_at	ATP-binding cassette, sub-family A, member 2	0.0085	-0.0607	0.4103	-0.1981	0.2286	2149 ± 243	2713 ± 235	3010 ± 268	3321 ± 773
203192_at	ATP-binding cassette, sub-family B, member 6	0.0382	-0.3080	-0.4790	0.4842	0.3859	381 ± 19	390 ± 40	364 ± 33	452 ± 51
203981_s_at	ATP-binding cassette, sub-family D, member 4	0.2780	-0.0112	0.4061	-0.0865	0.1593	316 ± 27	366 ± 25	341 ± 12	410 ± 54
202123_s_at	v-abl Abelson murine leukemia viral oncogene homolog 1	0.0018	-0.0247	0.4739	-0.4913	0.0929	989 ± 118	1154 ± 138	1371 ± 137	1561 ± 257
210461_s_at	actin binding LIM protein 1	0.0159	-0.0266	-0.4038	-0.2723	0.0624	96 ± 14	92 ± 20	132 ± 22	171 ± 31
202366_at	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	0.0128	-0.0019	0.0607	-0.1022	0.0042	161 ± 12	216 ± 16	253 ± 20	321 ± 53
203164_at	acyl-Coenzyme A transporter	0.2331	-0.0035	-0.3973	-0.0775	0.1115	343 ± 21	359 ± 14	382 ± 20	418 ± 28
204241_at	acyl-Coenzyme A oxidase 3, pristanoyl	0.2933	-0.0340	0.3973	0.1675	0.1455	274 ± 18	279 ± 25	304 ± 39	375 ± 43
207973_x_at	acrosomal vesicle protein 1	0.8153	-0.0215	0.0600	-0.0634	0.0397	220 ± 14	280 ± 25	247 ± 23	321 ± 32
208223_s_at	activin A receptor, type IB	0.0068	-0.0026	-0.4471	0.4256	0.0045	79 ± 13	93 ± 7	93 ± 13	167 ± 27
207953_at	neuronal thread protein	0.0006	-0.0147	-0.3379	-0.0562	0.0351	200 ± 17	235 ± 14	389 ± 71	383 ± 74
205745_x_at	a disintegrin and metalloproteinase domain 17	0.0227	-0.0249	-0.0299	-0.4591	0.0691	406 ± 31	389 ± 7	481 ± 30	470 ± 29
207665_at	a disintegrin and metalloproteinase domain 21	0.1526	-0.0427	0.4568	0.4805	0.0454	213 ± 22	281 ± 38	244 ± 25	334 ± 35
206134_at	ADAM-like, decysin 1	0.0693	-0.0210	0.2733	-0.4496	0.0092	55 ± 5	69 ± 8	105 ± 15	89 ± 10
202027_at	ADAMDEC1	0.1781	-0.0340	0.2568	-0.0761	0.2487	303 ± 31	323 ± 32	329 ± 36	411 ± 55
206848_at	ADAMTS9	0.0842	-0.0006	-0.1342	0.3729	0.0069	323 ± 56	316 ± 37	379 ± 45	545 ± 34
213217_at	double-stranded RNA specific adenosine deaminase	0.0034	-0.0137	0.4392	0.4272	0.0568	3323 ± 178	3330 ± 215	4453 ± 552	4496 ± 513
209320_at	adenylate cyclase 2	0.5995	-0.0169	0.1650	-0.2960	0.1846	543 ± 36	545 ± 39	622 ± 36	675 ± 74
203741_s_at	adenylate cyclase 3	0.0464	-0.0129	0.1193	-0.0061	0.1919	228 ± 33	311 ± 39	292 ± 20	340 ± 56
20753_s_at	adenylate cyclase 7	0.0071	-0.0032	0.0287	-0.0699	0.0009	4514 ± 321	5928 ± 566	8335 ± 749	7237 ± 742
205613_s_at	adducin 3	0.0069	-0.0201	0.2979	-0.0827	0.1403	48 ± 7	48 ± 10	79 ± 20	87 ± 16
207192_at	alcohol dehydrogenase IB, β polypeptide	0.0001	-0.0004	-0.1628	-0.2006	0.0085	293 ± 46	305 ± 48	530 ± 72	643 ± 123
218735_s_at	AE binding protein 1	0.0143	-0.2315	0.0427	-0.0670	0.3397	496 ± 25	506 ± 21	596 ± 66	564 ± 46
206840_at	zinc finger protein	0.0374	-0.0301	0.1782	0.4366	0.0124	98 ± 17	119 ± 18	105 ± 9	179 ± 22
221788_at	afatinib	0.8955	-0.0164	-0.1862	-0.0265	0.3263	259 ± 27	313 ± 56	322 ± 39	400 ± 80
219792_at	N-acetylglucosamine-phosphate mutase	0.0777	-0.0254	-0.3096	-0.4473	0.0649	214 ± 21	224 ± 24	229 ± 15	306 ± 36
32837_at	agnatline ureohydrolase	0.2503	-0.0078	0.1110	-0.0851	0.0766	468 ± 24	490 ± 44	556 ± 32	637 ± 79
217419_x_at	1-acylglycerol-3-phosphate O-acyltransferase 2	0.0265	-0.3160	0.0613	-0.3947	0.6315	554 ± 44	633 ± 80	652 ± 36	697 ± 143
205357_s_at	agrin	0.0017	-0.0003	0.1517	-0.0147	0.0075	79 ± 6	105 ± 14	122 ± 10	138 ± 14
213592_at	angiotensin II receptor, type 1	0.0444	-0.0459	0.0168	-0.0327	0.0253	897 ± 172	1599 ± 422	3549 ± 921	2433 ± 622
212543_at	angiotensin II receptor-like 1	0.1970	-0.0054	0.0184	-0.1655	0.0408	177 ± 19	215 ± 22	218 ± 13	289 ± 44
202587_s_at	absent in melanoma 1	0.0442	-0.0894	0.3108	-0.2714	0.4005	1489 ± 121	1525 ± 133	1768 ± 241	1863 ± 205
212172_at	adenylate kinase 1	0.0417	-0.1628	0.0649	-0.3466	0.1369	143 ± 15	134 ± 19	142 ± 20	243 ± 68
210674_s_at	adenylate kinase 2	0.0301	-0.8514	0.2896	-0.2216	0.8298	584 ± 36	634 ± 55	655 ± 65	622 ± 77
220204_s_at	A kinase anchor protein 1	0.0059	-0.0028	0.0412	-0.0187	0.0097	441 ± 42	513 ± 52	641 ± 79	869 ± 138
215483_at	A kinase anchor protein 13	0.1518	-0.0230	0.0412	-0.0231	0.0890	205 ± 45	275 ± 27	408 ± 75	354 ± 77
216594_x_at	A kinase anchor protein 9	0.3738	-0.0407	-0.0361	0.1419	0.0685	726 ± 75	639 ± 50	792 ± 22	876 ± 50
	aldo-keto reductase family 1, member C2									

Web Table 5 (1)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
209160_at	AKR1C3	aldo-keto reductase family 1, member C3	0.3544	-0.0084	-0.3514	-0.4961	0.0263	352 ± 49	324 ± 33	575 ± 67	538 ± 98
219393_s_at	AKT3	v-akt murine thymoma viral oncogene homolog 3	0.0257	-0.1261	0.0552	0.4652	0.1281	153 ± 15	199 ± 24	198 ± 24	243 ± 40
207016_s_at	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	0.0515	-0.0053	-0.0403	0.0805	0.0055	212 ± 27	157 ± 19	400 ± 70	569 ± 138
202054_s_at	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	0.5623	-0.0027	-0.0002	0.2161	0.0473	868 ± 46	750 ± 56	1014 ± 52	1217 ± 28
214220_s_at	ALMS1	Alstrom syndrome 1	0.0641	-0.0127	-0.0028	-0.0399	0.1605	160 ± 17	203 ± 18	228 ± 23	252 ± 52
210170_at	ALP	α-actinin-2-associated LIM protein	0.0597	-0.0185	0.0807	-0.3478	0.1315	76 ± 8	102 ± 14	95 ± 6	141 ± 37
202125_s_at	ALS2CR3	ALS 2 chromosome region, candidate 3	0.0046	-0.0169	0.3688	-0.1876	0.0515	1607 ± 144	1664 ± 150	2244 ± 194	2186 ± 295
203002_at	AMOTL2	angiomin like 2	0.0196	-0.0580	0.1666	-0.1487	0.2241	847 ± 58	1017 ± 115	1077 ± 60	1227 ± 231
207992_s_at	AMPD3	adenosine monophosphate deaminase	0.0317	-0.0129	0.1057	0.3435	0.0281	569 ± 37	683 ± 134	645 ± 52	933 ± 100
205609_at	ANGPT1	angiopoietin 1	0.0907	-0.0043	0.1258	-0.0190	0.1030	346 ± 42	388 ± 76	523 ± 89	556 ± 62
213004_at	ANGPTL2	angiopoietin-like 2	0.0000	-0.0393	0.0122	-0.1088	0.0460	98 ± 8	133 ± 15	161 ± 8	173 ± 35
201305_x_at	ANP32B	acidic nuclear phosphoprotein 32 family, member B	0.0029	-0.0014	0.2229	-0.0488	0.0179	720 ± 86	850 ± 111	1215 ± 197	1253 ± 11
201012_at	ANXA1	annexin A1	0.0169	-0.0043	0.3733	-0.2274	0.0704	309 ± 36	327 ± 48	654 ± 176	914 ± 296
213503_x_at	ANXA2	annexin A2	0.1193	-0.0147	-0.0311	0.4328	0.0689	1001 ± 119	878 ± 75	1011 ± 143	1423 ± 200
207064_s_at	AOC2	amine oxidase, copper containing 2	0.1172	-0.0414	0.0591	-0.2237	0.0121	216 ± 16	286 ± 25	225 ± 16	335 ± 43
200845_s_at	AOP2	anti-oxidant protein 2	0.0819	-0.0387	0.0292	-0.4848	0.0547	2495 ± 180	2674 ± 239	4147 ± 588	3524 ± 606
205423_at	AP1B1	adaptor-related protein complex 1, β 1 subunit	0.0366	-0.1486	-0.3909	-0.2217	0.2246	340 ± 35	314 ± 32	424 ± 34	407 ± 64
202398_at	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	0.0262	-0.0250	-0.4886	-0.4378	0.1517	70 ± 13	81 ± 20	88 ± 23	134 ± 24
215148_s_at	APBA3	amyloid β precursor protein-binding, family A, member 3	0.0481	-0.1362	-0.2320	0.2067	0.1586	469 ± 41	464 ± 73	479 ± 49	663 ± 108
218555_at	APC2	anaphase-promoting complex subunit 2	0.0418	-0.0709	0.1166	0.1431	0.0825	620 ± 120	544 ± 79	592 ± 41	1054 ± 246
220237_at	APG3	autophagy Apg3p/Autp1-like	0.0750	-0.0209	0.0384	-0.1811	0.0440	60 ± 7	50 ± 9	91 ± 10	127 ± 38
204902_s_at	Apg4B	KIAA0943 protein	0.6193	-0.0411	-0.1332	-0.1610	0.0855	353 ± 38	304 ± 54	328 ± 25	470 ± 63
207175_at	APM1	adipose most abundant gene transcript 1	0.0615	-0.0426	0.4119	0.3825	0.3306	83 ± 12	91 ± 19	111 ± 19	133 ± 32
207158_at	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic polypep. 1	0.2954	-0.0074	-0.2239	-0.2207	0.0481	157 ± 27	160 ± 29	155 ± 8	263 ± 43
213553_x_at	APOC1	apolipoprotein C-I	0.2519	-0.0489	0.0396	-0.3988	0.1150	1261 ± 161	1713 ± 237	1606 ± 135	1865 ± 143
206738_at	APOC4	apolipoprotein C-IV	0.0014	-0.0267	0.0024	-0.2108	0.0482	179 ± 11	235 ± 25	281 ± 13	305 ± 60
221013_s_at	APOL2	apolipoprotein L, 2	0.1087	-0.0013	0.0910	-0.0378	0.0066	162 ± 20	180 ± 13	256 ± 17	250 ± 30
211277_x_at	APP	amyloid β precursor protein	0.0085	-0.0024	0.0521	-0.0046	0.0319	345 ± 18	385 ± 28	458 ± 24	573 ± 108
218527_at	APTX	apoptaxin	0.0130	-0.3520	-0.3766	0.4755	0.8193	700 ± 39	688 ± 57	730 ± 57	761 ± 79
209047_at	AQP1	aquaporin 1	0.1381	-0.0162	0.4508	-0.3638	0.1509	3845 ± 804	3974 ± 762	1294 ± 1026	6422 ± 799
216219_at	AQP6	aquaporin 6, kidney specific	0.1343	-0.0479	0.2267	-0.1735	0.1153	339 ± 30	340 ± 18	349 ± 40	482 ± 77
203025_at	ARD1	ARD1 homolog, N-acetyltransferase	0.0212	-0.0851	0.3202	-0.4038	0.2991	525 ± 41	498 ± 49	577 ± 55	692 ± 126
214182_at	ARF6	ADP-ribosylation factor 6	0.1885	-0.0027	0.3874	-0.0262	0.0753	143 ± 10	128 ± 26	181 ± 23	190 ± 11
217888_s_at	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	0.2345	-0.0486	0.1206	-0.0101	0.3263	602 ± 43	658 ± 36	744 ± 76	735 ± 84
203945_at	ARG2	arginase, type II	0.0321	-0.0063	0.2004	-0.4407	0.0071	320 ± 20	355 ± 24	371 ± 20	492 ± 57
57082_at	ARH	LDL receptor adaptor protein	0.0483	-0.0508	-0.3702	0.3490	0.0559	422 ± 44	473 ± 114	441 ± 66	799 ± 173
202117_at	ARHGAP1	Rho GTPase activating protein 1	0.0243	-0.0543	0.1319	0.3211	0.1404	2789 ± 229	3196 ± 376	3283 ± 271	4023 ± 573
206167_s_at	ARHGAP6	Rho GTPase activating protein 6	0.1337	-0.0476	0.1965	0.2431	0.1326	348 ± 31	377 ± 58	457 ± 20	486 ± 66
216620_s_at	ARHGEF10	Rho guanine nucleotide exchange factor 10	0.0020	-0.0082	0.2725	-0.4057	0.0305	654 ± 67	765 ± 91	946 ± 70	921 ± 69
217348_x_at	ARHGEF15	Rho guanine nucleotide exchange factor 15	0.5720	-0.0164	0.0480	-0.0151	0.0821	199 ± 18	235 ± 31	226 ± 24	285 ± 30
208009_s_at	ARHGEF16	Rho guanine nucleotide exchange factor 16	0.0199	-0.0043	0.2112	-0.2052	0.0149	173 ± 25	176 ± 17	276 ± 27	291 ± 46
201954_at	ARPC1B	actin related protein 23 complex, subunit 1B, 41kDa	0.0177	-0.0194	0.0218	-0.2238	0.1227	394 ± 26	492 ± 59	536 ± 56	553 ± 53

Web Table 5 (2)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
222047_s_at	ARS2	arsenate resistance protein ARS2	0.0099	-0.0053	0.4491	-0.4489	0.0706	1624 ± 85	1755 ± 149	2029 ± 163	2187 ± 203
210385_s_at	ARTS-1	type 1 TNF receptor shedding aminopeptidase regulator	0.1149	-0.0082	0.3852	-0.0417	0.1942	187 ± 26	189 ± 29	215 ± 10	267 ± 36
212818_s_at	ASB1	ankyrin repeat and SOCS box-containing 1	0.1412	-0.0108	0.3778	0.3963	0.0806	821 ± 40	783 ± 30	853 ± 51	999 ± 91
209987_s_at	ASCL1	achaete-scute complex-like 1	0.0416	-0.0042	0.0197	-0.1938	0.0184	353 ± 37	537 ± 111	502 ± 78	832 ± 153
204244_s_at	ASK	activator of S phase kinase	0.8717	-0.0304	0.0294	-0.2094	0.3078	107 ± 7	97 ± 10	110 ± 7	126 ± 14
208033_s_at	ATBF1	AT-binding transcription factor 1	0.0528	-0.0240	0.0612	-0.0685	0.0416	140 ± 25	176 ± 20	243 ± 23	206 ± 33
204998_s_at	ATF5	activating transcription factor 5	0.0079	-0.0980	0.1389	0.4472	0.0816	216 ± 19	280 ± 46	289 ± 10	320 ± 29
212096_s_at	ATIP1	AT2 receptor-interacting protein 1	0.3979	-0.0223	-0.0549	-0.3781	0.2176	2852 ± 258	2849 ± 463	3344 ± 306	3342 ± 227
213238_at	ATP10D	ATPase, Class V, type 10D	0.1324	-0.0307	0.0384	-0.2089	0.2592	289 ± 19	297 ± 28	317 ± 35	370 ± 39
214150_x_at	ATP6V0E	ATPase, H ⁺ -transporting, lysosomal 9kDa, V0 subunit e	0.0085	-0.0001	-0.4607	-0.1644	0.0069	3051 ± 293	2997 ± 267	3623 ± 256	4448 ± 364
205198_s_at	ATP7A	ATPase, Cu ⁺ -transporting, α polypeptide	0.0026	-0.0015	0.1093	-0.0686	0.0141	232 ± 19	276 ± 21	297 ± 17	365 ± 47
214594_x_at	ATP8B1	ATPase, Class I, type 8B, member 1	0.0061	-0.0400	0.2453	-0.0306	0.0561	1259 ± 205	1462 ± 119	2399 ± 338	2176 ± 551
206251_s_at	AVPR1A	arginine vasopressin receptor 1A	0.0103	-0.0048	-0.0548	0.2142	0.0134	54 ± 4	52 ± 8	68 ± 11	101 ± 17
209309_at	AZGP1	α-2-glycoprotein 1, zinc	0.1755	-0.0020	-0.1857	-0.1359	0.0582	148 ± 32	153 ± 22	250 ± 71	301 ± 30
209413_at	B4GALT2	UDP β 1,4-galactosyltransferase	0.0150	-0.2865	-0.3149	0.0217	0.2782	637 ± 30	571 ± 77	710 ± 42	764 ± 116
202974_x_at	BA108L7.2	similar to rat frataxin carrier-like protein	0.0450	-0.8301	0.1331	0.4391	0.1871	1030 ± 60	1094 ± 91	1268 ± 92	1085 ± 83
221234_s_at	BACH2	basic leucine zipper transcription factor 2	0.1147	-0.0124	0.4399	-0.4112	0.1052	314 ± 25	350 ± 36	366 ± 24	424 ± 38
209364_at	BAD	BCL2-antagonist of cell death	0.0183	-0.0380	0.2296	0.2838	0.2043	544 ± 37	561 ± 60	680 ± 49	749 ± 140
202666_s_at	BAF53A	BAF53	0.6228	-0.0222	-0.4574	-0.1521	0.2152	235 ± 30	269 ± 26	314 ± 41	314 ± 22
202387_at	BAG1	BCL2-associated athanogene	0.1238	-0.0437	0.1509	-0.0546	0.2868	746 ± 29	745 ± 68	767 ± 58	876 ± 56
213105_s_at	BAIAP3	BAI1-associated protein 3	0.1084	-0.0263	0.0289	-0.4828	0.1003	312 ± 19	353 ± 48	382 ± 25	433 ± 42
218966_x_at	BANP	BTG3 associated nuclear protein	0.0630	-0.0020	-0.1251	-0.3183	0.0276	525 ± 24	452 ± 75	495 ± 59	801 ± 140
217986_s_at	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	0.4382	-0.0466	-0.1131	-0.3254	0.5147	191 ± 29	174 ± 24	201 ± 23	238 ± 37
201353_s_at	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	0.0022	-0.1658	-0.0797	-0.1746	0.3146	275 ± 31	246 ± 16	376 ± 41	362 ± 103
203080_s_at	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	0.0015	-0.0049	-0.2754	-0.2383	0.0749	1215 ± 117	1277 ± 148	1528 ± 109	1748 ± 230
214139_at	BCAA	RBP1-like protein	0.8617	-0.0325	-0.4738	-0.3532	0.2877	133 ± 12	139 ± 19	149 ± 13	178 ± 24
221623_at	SCAN	chondroitin sulfate proteoglycan BEHAB/brevican	0.0537	-0.0052	-0.4303	-0.4111	0.0674	378 ± 29	374 ± 31	496 ± 63	529 ± 58
203576_at	BCAT2	branched chain aminotransferase 2, mitochondrial	0.0107	-0.0089	0.4821	-0.0728	0.1003	428 ± 50	453 ± 50	538 ± 35	585 ± 56
204872_at	BCE-1	BCE-1 protein	0.0987	-0.0433	-0.1150	-0.2518	0.3342	2317 ± 176	2238 ± 310	2563 ± 176	2812 ± 276
203685_at	BCL2	B-cell CLL/lymphoma 2	0.0206	-0.0003	-0.1509	0.2748	0.0021	992 ± 105	821 ± 72	1193 ± 141	1514 ± 79
203140_at	BCL6	B-cell CLL/lymphoma 6	0.0984	-0.0029	-0.1477	-0.1755	0.0958	3035 ± 407	3028 ± 315	3862 ± 668	4927 ± 811
210679_x_at	BCL7A	B-cell CLL/lymphoma 7A	0.0260	-0.0016	0.0430	-0.0731	0.0023	744 ± 103	784 ± 87	1431 ± 127	1264 ± 198
218056_at	BFAR	bifunctional apoptosis regulator	0.0001	-0.0056	-0.3329	0.4813	0.0177	425 ± 21	395 ± 9	490 ± 39	590 ± 71
206956_at	BGLAP	bone γ-carboxyglutamate protein	0.0015	-0.1275	0.2620	-0.1442	0.4224	135 ± 18	150 ± 10	174 ± 25	190 ± 40
202761_x_at	BGN	biglycan	0.0134	-0.0022	0.0318	-0.0015	0.0133	424 ± 33	557 ± 32	544 ± 47	717 ± 94
203278_s_at	BHC80	BRAF35HDAC2 complex	0.0622	-0.0421	-0.0036	0.2633	0.0148	568 ± 82	407 ± 24	683 ± 70	666 ± 43
219902_at	BHMT2	βine-homocysteine methyltransferase 2	0.0027	-0.7079	0.4322	0.0813	0.4214	75 ± 11	94 ± 22	131 ± 28	104 ± 31
214716_at	BIKE	BMP-2 inducible kinase	0.0251	-0.5080	0.1746	-0.3795	0.4249	96 ± 10	98 ± 7	122 ± 7	115 ± 21
214643_x_at	BIN1	bridging integrator 1	0.0007	-0.0351	0.3823	-0.4420	0.0697	889 ± 59	1098 ± 196	1079 ± 142	1619 ± 310
222199_s_at	BIN3	bridging integrator 3	0.0243	-0.1004	-0.0655	-0.1899	0.0066	417 ± 14	384 ± 39	553 ± 44	463 ± 26
204861_s_at	BIRC1	baculoviral IAP repeat-containing 1	0.0089	-0.0287	0.0822	-0.2118	0.0917	235 ± 39	308 ± 38	323 ± 52	439 ± 85
202076_at	BIRC2	baculoviral IAP repeat-containing 2	0.1764	-0.0004	-0.2373	-0.2328	0.0047	1322 ± 44	1230 ± 81	1333 ± 92	1672 ± 103

Web Table 5 (3)

Probe set Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
219520_s_at	BM042	0.1508	-0.0118	0.3688	-0.1907	0.0557	675 ± 74	871 ± 109	841 ± 46	1007 ± 98
208292_at	BMP10	0.1511	-0.0399	-0.0343	0.2072	0.1133	182 ± 18	157 ± 14	198 ± 18	233 ± 30
213578_at	BMPR1A	0.1070	-0.0081	0.4084	-0.2047	0.1331	558 ± 47	601 ± 38	716 ± 85	769 ± 94
215016_x_at	BPAG1	0.0534	-0.0039	-0.4014	-0.2492	0.0282	5282 ± 187	5147 ± 325	6388 ± 444	6107 ± 310
220142_at	BRAL1	0.0405	-0.0038	-0.1426	0.3367	0.0011	510 ± 40	372 ± 71	446 ± 41	888 ± 149
213473_at	BRAP	0.0364	-0.0024	0.0192	-0.0153	0.0087	177 ± 16	231 ± 19	241 ± 11	253 ± 17
204531_s_at	BRCA1	0.0108	-0.0747	0.2849	0.3185	0.1295	94 ± 11	128 ± 23	149 ± 22	154 ± 24
204520_x_at	BRD1	0.1618	-0.0103	0.2763	-0.0170	0.0053	556 ± 49	617 ± 46	776 ± 16	675 ± 36
214911_s_at	BRD2	0.0253	-0.0489	-0.4958	0.4433	0.2672	1066 ± 126	1052 ± 94	1268 ± 111	1341 ± 30
203825_at	BRD3	0.0019	-0.0499	0.1745	-0.3258	0.1166	1333 ± 129	1593 ± 221	2030 ± 210	2257 ± 25
202103_at	BRD4	0.0042	-0.0008	0.4088	-0.2915	0.0064	358 ± 36	338 ± 19	434 ± 27	520 ± 46
204481_at	BRPF1	0.0119	-0.0021	0.3547	-0.1542	0.0183	256 ± 38	308 ± 40	316 ± 25	456 ± 64
207369_at	BR3	0.0584	-0.0210	0.0075	-0.0861	0.0734	119 ± 14	145 ± 15	163 ± 26	210 ± 32
203542_s_at	BTEB1	0.0045	-0.0004	-0.3359	-0.0642	0.0033	493 ± 48	485 ± 59	611 ± 49	857 ± 17
201236_s_at	BTG2	0.0738	-0.0134	-0.3544	-0.4104	0.0727	772 ± 86	791 ± 44	809 ± 50	1051 ± 14
215425_at	BTG3	0.0290	-0.0044	0.0825	0.4505	0.0091	92 ± 6	120 ± 15	135 ± 16	175 ± 26
204821_at	BTNSA3	0.4096	-0.0381	0.4254	-0.1324	0.3087	96 ± 18	93 ± 20	127 ± 16	146 ± 33
217207_s_at	BTNL3	0.0425	-0.0474	-0.3797	-0.1285	0.2296	302 ± 24	303 ± 34	323 ± 24	391 ± 48
216091_s_at	BTRC	0.1195	-0.0202	-0.2478	0.4764	0.0933	197 ± 18	189 ± 11	201 ± 13	247 ± 20
202096_s_at	BZRP	0.3296	-0.0440	-0.3461	-0.2356	0.4039	627 ± 65	620 ± 74	674 ± 61	767 ± 59
217928_s_at	C11orf23	0.5503	-0.0417	-0.2945	0.4476	0.1577	617 ± 42	520 ± 25	624 ± 30	685 ± 69
204073_s_at	C11orf9	0.0046	-0.0116	-0.4375	0.3976	0.0567	1722 ± 260	1813 ± 253	2488 ± 293	3448 ± 814
218374_s_at	C12orf4	0.3940	-0.0368	0.2320	-0.4711	0.1436	343 ± 13	323 ± 24	342 ± 17	403 ± 37
218183_at	C16orf5	0.0024	-0.0003	0.4460	-0.2017	0.0116	307 ± 23	318 ± 27	368 ± 25	505 ± 75
209574_s_at	C18orf1	0.8664	-0.0129	0.4174	-0.4672	0.0309	341 ± 12	330 ± 28	301 ± 13	479 ± 78
213390_at	C19orf7	0.0016	-0.1056	0.1669	-0.4800	0.2720	995 ± 72	1134 ± 143	1286 ± 121	1340 ± 210
209883_at	C1orf17	0.3038	-0.0320	0.4297	0.3759	0.2095	1089 ± 88	1156 ± 104	1180 ± 78	1396 ± 143
220992_s_at	C1orf25	0.7491	-0.0408	0.3573	-0.0364	0.1346	177 ± 12	194 ± 27	175 ± 8	234 ± 24
212067_s_at	C1R	0.7171	-0.0331	-0.1028	0.3522	0.2474	287 ± 49	260 ± 41	283 ± 27	390 ± 58
208747_s_at	C1S	0.0210	-0.0118	-0.1632	-0.1282	0.0419	442 ± 55	424 ± 54	793 ± 167	739 ± 120
207482_at	C20orf10	0.0423	-0.0337	0.1532	0.3122	0.0355	149 ± 16	146 ± 19	168 ± 12	274 ± 61
209422_at	C20orf104	0.1491	-0.0113	0.0243	-0.0391	0.1277	882 ± 55	1015 ± 77	1019 ± 38	1102 ± 76
209020_at	C20orf111	0.1097	-0.0411	-0.2008	0.3022	0.1830	392 ± 14	373 ± 24	419 ± 30	461 ± 42
208880_s_at	C20orf14	0.0087	-0.7205	0.0539	0.4275	0.6000	304 ± 26	385 ± 67	342 ± 28	421 ± 112
218010_x_at	C20orf149	0.0490	-0.0527	0.1466	-0.4514	0.1982	683 ± 80	738 ± 77	806 ± 27	979 ± 168
210357_s_at	C20orf16	0.0002	-0.0030	0.2860	-0.0934	0.0111	904 ± 84	1144 ± 80	1239 ± 89	1440 ± 166
221827_at	C20orf18	0.0144	-0.0221	0.0456	0.2796	0.0226	430 ± 28	456 ± 22	456 ± 64	622 ± 19
218586_at	C20orf20	0.0107	-0.4800	0.4614	0.4958	0.5419	379 ± 37	393 ± 45	458 ± 40	442 ± 61
219706_at	C20orf29	0.4606	-0.0206	0.1750	-0.3770	0.0785	485 ± 19	480 ± 41	504 ± 31	628 ± 71
218089_at	C20orf4	0.1009	-0.0044	-0.4318	-0.3579	0.0095	622 ± 24	666 ± 40	680 ± 36	833 ± 62
218145_at	C20orf87	0.0014	-0.0047	0.1287	-0.3686	0.0052	327 ± 21	340 ± 31	314 ± 32	492 ± 56
203986_s_at	C21orf2	0.0190	-0.0308	-0.3788	0.3050	0.0283	274 ± 27	257 ± 26	298 ± 18	412 ± 64

Web Table 5 (4)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
220543_at	C21orf62	chromosome 21 open reading frame 62	0.1357	-0.0089	0.4862	0.1216	0.0030	125 ± 17	124 ± 14	127 ± 12	217 ± 26
220941_s_at	C21orf91	chromosome 21 open reading frame 91	0.0011	-0.0087	-0.1983	-0.3222	0.0057	153 ± 26	151 ± 18	155 ± 11	302 ± 56
217622_at	C22orf3	chromosome 22 open reading frame 3	0.0401	-0.0221	0.0616	-0.0160	0.0752	120 ± 10	142 ± 29	204 ± 35	241 ± 52
216305_s_at	C2orf3	chromosome 2 open reading frame 3	0.1514	-0.0289	0.0619	-0.2066	0.1066	193 ± 12	256 ± 30	256 ± 20	278 ± 36
201298_s_at	C2orf6	chromosome 2 open reading frame 6	0.0060	-0.1575	-0.2365	-0.2771	0.6045	307 ± 23	271 ± 37	304 ± 48	356 ± 60
214428_x_at	C4A	complement component 4A	0.0169	-0.0024	-0.4946	-0.1759	0.0361	2009 ± 348	2233 ± 417	2694 ± 281	3836 ± 692
208451_s_at	C4B	complement component 4B	0.0417	-0.0115	0.4895	0.3056	0.0518	2358 ± 463	1849 ± 298	2910 ± 305	3553 ± 440
205500_at	C5	complement component 5	0.0406	-0.1233	0.2302	-0.0336	0.2194	183 ± 14	212 ± 19	240 ± 21	245 ± 38
48031_t_at	C5orf4	chromosome 5 open reading frame 4	0.0116	-0.1182	0.0422	-0.3703	0.0303	543 ± 35	755 ± 125	768 ± 54	975 ± 157
221766_s_at	C6orf37	chromosome 6 open reading frame 37	0.0579	-0.0121	0.1136	-0.0463	0.1911	184 ± 31	240 ± 41	285 ± 32	303 ± 57
208469_s_at	C6orf8	chromosome 6 open reading frame 8	0.0141	-0.2490	0.0712	0.4707	0.4058	138 ± 19	192 ± 46	190 ± 24	247 ± 74
204265_s_at	C6orf9	chromosome 6 open reading frame 9	0.0431	-0.0024	0.0892	-0.0046	0.0429	408 ± 44	471 ± 31	547 ± 41	623 ± 7
202992_at	C7	complement component 7	0.0004	-0.0114	0.0940	-0.0771	0.1185	65 ± 12	76 ± 15	117 ± 28	126 ± 20
212247_at	C7orf14	chromosome 7 open reading frame 14	0.0838	-0.0103	-0.3710	-0.1692	0.0079	277 ± 18	330 ± 27	289 ± 13	388 ± 29
204024_at	C8orf1	chromosome 8 open reading frame 1	0.0076	-0.0220	0.1528	-0.1242	0.0526	251 ± 15	259 ± 33	259 ± 26	347 ± 30
221543_s_at	C8orf2	chromosome 8 open reading frame 2	0.1488	-0.0194	0.0309	-0.1725	0.2136	763 ± 76	839 ± 29	884 ± 30	938 ± 58
212848_s_at	C9orf3	chromosome 9 open reading frame 3	0.0365	-0.0171	0.3396	0.4588	0.1084	545 ± 55	648 ± 106	724 ± 73	818 ± 71
61874_at	C9orf7	chromosome 9 open reading frame 7	0.1132	-0.0001	0.0699	-0.0607	0.0067	678 ± 33	815 ± 53	848 ± 36	1030 ± 106
205949_at	CA1	carbonic anhydrase I	0.1709	-0.0334	-0.4004	-0.3545	0.1119	170 ± 23	165 ± 11	170 ± 19	239 ± 34
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex like	0.0030	-0.0629	-0.2588	-0.2545	0.1607	647 ± 36	722 ± 51	722 ± 51	836 ± 84
210770_s_at	CACNA1A	P/Q type calcium channel, α 1A subunit	0.0296	-0.1755	-0.3549	0.0190	0.0739	842 ± 86	600 ± 108	824 ± 171	1334 ± 285
210380_s_at	CACNA1G	calcium channel, voltage-dependent, α 1G subunit	0.0369	-0.6883	0.3657	-0.1288	0.9121	110 ± 16	110 ± 31	129 ± 18	118 ± 26
214880_x_at	CALD1	caldesmon 1	0.1284	-0.0197	0.0449	-0.0126	0.1927	103 ± 8	146 ± 15	162 ± 10	160 ± 42
213956_at	CAP350	centrosome-associated protein 350	0.0676	-0.0213	0.0893	-0.0111	0.0257	326 ± 44	357 ± 29	624 ± 83	501 ± 116
210944_s_at	CAPN3	calpain 3	0.0344	-0.0585	0.4311	-0.3479	0.2365	1953 ± 281	2232 ± 473	2295 ± 305	3153 ± 613
21207_s_at	CAPRI	Ca ²⁺ -promoted Ras inactivator	0.0063	-0.1193	0.0917	-0.0768	0.2382	213 ± 17	286 ± 28	357 ± 64	341 ± 84
212512_s_at	CARM1	coactivator-associated arginine methyltransferase-1	0.0025	-0.1770	0.2979	0.0375	0.2178	825 ± 28	888 ± 121	966 ± 109	1186 ± 210
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase	0.0015	-0.0229	0.3791	-0.4989	0.1543	625 ± 45	619 ± 53	711 ± 59	780 ± 62
61297_at	CASKIN2	calc-interacting protein 2	0.0358	-0.1118	0.3470	-0.1709	0.0343	185 ± 25	211 ± 9	296 ± 25	241 ± 38
202763_at	CASP3	caspase 3, apoptosis-related cysteine protease	0.4648	-0.0042	-0.0319	0.2221	0.0154	244 ± 13	214 ± 14	256 ± 21	335 ± 43
213596_at	CASP4	caspase 4, apoptosis-related cysteine protease	0.0155	-0.0002	0.1019	-0.0769	0.0099	123 ± 9	146 ± 21	159 ± 14	206 ± 19
211464_x_at	CASP6	caspase 6, apoptosis-related cysteine protease	0.0005	-0.0328	0.2753	-0.0058	0.1579	104 ± 17	143 ± 17	189 ± 36	206 ± 19
210775_x_at	CASP9	caspase 9, apoptosis-related cysteine protease	0.0351	-0.0070	-0.1949	-0.1976	0.0296	524 ± 29	542 ± 27	530 ± 26	649 ± 41
212586_at	CAST	calpastatin	0.2280	-0.0017	0.0618	-0.0001	0.0236	947 ± 34	1222 ± 104	1143 ± 61	1316 ± 113
202370_s_at	CBFB	core-binding factor, β subunit	0.1357	-0.0129	-0.1676	0.4655	0.2039	2103 ± 223	2117 ± 130	2462 ± 234	2647 ± 193
209682_at	CBLB	Cas-Bi-M ecotropic retroviral transforming sequence b	0.0047	-0.0019	-0.2344	0.4864	0.0211	271 ± 27	255 ± 13	308 ± 25	384 ± 43
206559_x_at	CCND1	cyclin D1	0.0377	-0.1808	-0.2346	-0.4917	0.4216	8340 ± 1675	18791 ± 961	1418 ± 1318	0668 ± 1887
201700_at	CCND3	cyclin D3	0.0115	-0.0099	0.4261	0.4103	0.0202	1297 ± 62	1238 ± 81	1306 ± 110	1645 ± 106
208656_s_at	CCNI	cyclin I	0.1799	-0.0493	-0.0681	0.4341	0.1501	5148 ± 233	5220 ± 474	5192 ± 262	6191 ± 455
220871_at	CCRN4L	CCRN4 carbon catabolite repression 4-like	0.1917	-0.0279	0.0808	-0.0514	0.2738	317 ± 34	337 ± 33	388 ± 35	448 ± 84
215049_x_at	CD163	CD163 antigen	0.6135	-0.0102	-0.0945	-0.3960	0.1006	422 ± 84	361 ± 61	481 ± 81	689 ± 125
208405_s_at	CD164	CD164 antigen, sialomucin	-0.9469	-0.0441	-0.2522	-0.0675	0.6400	2494 ± 162	2415 ± 235	2474 ± 206	2795 ± 276

Web Table 5 (5)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
205789_at	CD1D	CD1D antigen, d polypeptide	0.9905	-0.0477	0.2226	-0.3644	0.0753	52 ± 13	61 ± 8	41 ± 8	93 ± 21
207995_s_at	CD209L	CD209 antigen-like	0.2358	-0.0036	0.0604	-0.0713	0.0090	111 ± 9	130 ± 9	129 ± 14	193 ± 28
204581_at	CD22	CD22 antigen	0.1308	-0.0166	-0.2997	-0.4034	0.0705	206 ± 46	223 ± 44	435 ± 90	370 ± 89
202256_at	CD2BP2	CD2 antigen binding protein 2	0.0003	-0.0044	-0.4117	-0.4526	0.0071	365 ± 20	382 ± 34	411 ± 28	523 ± 43
204192_at	CD37	CD37 antigen	0.0393	-0.0287	0.2019	-0.2060	0.1453	141 ± 21	185 ± 33	180 ± 30	234 ± 26
212014_x_at	CD44	CD44 antigen	0.1574	-0.0011	-0.3565	-0.0400	0.0245	202 ± 43	251 ± 42	345 ± 58	450 ± 76
205173_x_at	CD58	CD58 antigen	-0.6922	-0.0360	0.4973	-0.0105	0.6313	204 ± 23	219 ± 42	205 ± 38	270 ± 58
211189_x_at	CD84	CD84 antigen	0.4477	-0.0468	0.2165	-0.1569	0.1496	203 ± 21	245 ± 34	228 ± 16	286 ± 34
205685_at	CD86	CD86 antigen	0.1727	-0.0199	0.0656	-0.1265	0.2488	135 ± 25	183 ± 33	174 ± 19	226 ± 46
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A	0.0944	-0.0002	0.0000	-0.0166	0.0313	51 ± 5	68 ± 8	72 ± 8	90 ± 17
209658_at	CDC16	CDC16 cell division cycle 16 homolog	0.0049	-0.0551	-0.0478	0.3723	0.1444	1445 ± 138	1318 ± 118	1536 ± 90	2047 ± 400
201653_s_at	CDC25B	cell division cycle 25B	0.0444	-0.0807	-0.0429	-0.3220	0.5325	681 ± 75	687 ± 43	761 ± 57	795 ± 64
212401_s_at	CDC2L1	cell division cycle 2-like 1	0.0008	-0.0044	-0.3227	-0.3547	0.0464	841 ± 72	826 ± 55	979 ± 76	1162 ± 134
210473_s_at	CDC2L2	cell division cycle 2-like 2	0.0022	-0.0040	0.0912	-0.0263	0.0661	718 ± 34	845 ± 83	1021 ± 146	1119 ± 136
210965_x_at	CDC2L5	cell division cycle 2-like 5	0.0222	-0.0848	-0.3203	0.0448	0.0795	55 ± 12	42 ± 13	67 ± 11	90 ± 14
212540_at	CDC34	cell division cycle 34	0.0010	-0.0076	0.1914	-0.4305	0.0154	661 ± 28	673 ± 53	792 ± 34	824 ± 33
214721_x_at	CDC42EP4	CDC42 effector protein 4	0.0425	-0.0042	0.0381	-0.0265	0.1068	845 ± 77	1065 ± 139	1164 ± 62	1311 ± 225
209057_x_at	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	0.3540	-0.0401	0.0015	-0.0797	0.1905	325 ± 20	385 ± 31	375 ± 41	437 ± 43
203968_s_at	CDC6	CDC6 cell division cycle 6 homolog	0.0137	-0.2598	-0.2975	-0.2560	0.1934	95 ± 6	77 ± 14	112 ± 10	104 ± 15
206866_at	CDH4	cadherin 4, type 1, R-cadherin	0.0222	-0.0089	0.2027	0.2995	0.0126	409 ± 43	350 ± 20	553 ± 36	583 ± 76
201753_s_at	CDIPT	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	0.0092	-0.0557	0.1247	0.0875	0.0743	2104 ± 169	2319 ± 354	2368 ± 132	3127 ± 376
203468_at	CDK10	cyclin-dependent kinase 10	0.0024	-0.1007	-0.4625	0.1474	0.1340	219 ± 33	183 ± 32	282 ± 38	298 ± 43
204252_at	CDK2	cyclin-dependent kinase 2	0.7921	-0.0196	-0.1799	-0.3622	0.2063	325 ± 48	340 ± 31	349 ± 23	441 ± 49
201938_at	CDK2AP1	CDK2-associated protein 1	0.4430	-0.0078	0.3673	-0.0038	0.2039	6126 ± 401	6628 ± 886	1130 ± 1006	8106 ± 951
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C	0.8162	-0.0347	-0.3622	-0.1172	0.1428	3177 ± 375	2602 ± 246	3068 ± 430	4329 ± 776
204159_at	CDKN2C	cyclin-dependent kinase inhibitor 2C	0.0401	-0.1038	0.0184	0.4440	0.1807	382 ± 44	488 ± 60	500 ± 54	600 ± 96
204039_at	CEBPA	CCAAT/enhancer binding protein, α	0.0472	-0.1038	0.0184	0.4440	0.1807	597 ± 48	774 ± 100	786 ± 93	830 ± 61
213006_at	CEBPD	CCAAT/enhancer binding protein, δ	0.0539	-0.0127	-0.3282	0.3574	0.0041	77 ± 6	76 ± 7	78 ± 13	126 ± 12
212437_at	CENPB	centromere protein B, 80kDa	0.0025	-0.1993	0.0900	-0.2449	0.2886	360 ± 40	459 ± 67	540 ± 52	520 ± 126
90285_at	CENTA1	centaurin, α 1	0.0446	-0.3566	0.2010	0.0866	0.3929	3918 ± 394	4256 ± 851	4261 ± 531	5753 ± 1312
212477_at	CENTB2	centaurin, β 2	0.3075	-0.0126	-0.4842	0.3100	0.0529	75 ± 9	69 ± 8	87 ± 5	106 ± 13
214102_at	CENTD1	centaurin, δ 1	0.0066	-0.0098	0.0096	-0.1393	0.0116	395 ± 32	628 ± 62	696 ± 60	790 ± 141
34206_at	CENTD2	centaurin, δ 2	0.0114	-0.0714	-0.2073	0.4744	0.2501	506 ± 64	510 ± 62	642 ± 28	715 ± 148
219746_at	CERD4	cer-d4 homolog	0.0166	-0.0006	0.0173	0.4469	0.0000	284 ± 13	424 ± 62	382 ± 25	599 ± 35
211862_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	0.0529	-0.0129	0.0302	-0.0682	0.2689	270 ± 13	291 ± 33	329 ± 41	345 ± 18
48580_at	CGBP	CpG binding protein	0.0069	-0.1018	-0.3274	0.4843	0.3010	1841 ± 118	1982 ± 213	2086 ± 136	2326 ± 263
206861_s_at	CGGBP1	CGG triplet repeat binding protein 1	0.0712	-0.0006	0.2764	0.4898	0.0007	747 ± 47	698 ± 64	792 ± 58	1250 ± 152
212407_at	CGI-01	CGI-01 protein	0.0366	-0.0269	0.1279	-0.0781	0.0212	417 ± 19	453 ± 35	422 ± 12	537 ± 43
202938_x_at	CGI-96	CGI-96 protein	0.0377	-0.1320	-0.1858	-0.1763	0.2128	189 ± 10	150 ± 24	188 ± 30	251 ± 53
214273_x_at	CGTHBA	Conserved gene telomeric to α globin cluster	0.0751	-0.0216	-0.3683	0.4655	0.1113	512 ± 53	499 ± 29	633 ± 42	749 ± 140
206932_at	CH25H	cholesterol 25-hydroxylase	0.3227	-0.0402	0.4733	0.2922	0.1271	214 ± 38	224 ± 20	211 ± 25	355 ± 82
204258_at	CHD1	chromodomain helicase DNA binding protein 1	0.0430	-0.0665	-0.3121	0.4113	0.1449	327 ± 17	334 ± 18	395 ± 32	374 ± 22

Web Table 5 (6)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
203461_at	CHD2	chromodomain helicase DNA binding protein 2	0.0015	-0.0001	0.1545	-0.0180	0.0000	143 ± 11	178 ± 33	184 ± 21	352 ± 35
205022_s_at	CHES1	checkpoint suppressor 1	0.0476	-0.0093	-0.1288	-0.2885	0.1187	298 ± 34	265 ± 37	363 ± 44	400 ± 48
218803_at	CHFR	checkpoint with forkhead and ring finger domains	0.0342	-0.0316	0.1311	0.0361	0.0612	717 ± 33	782 ± 80	890 ± 35	1000 ± 12
220210_at	CHRNA10	cholinergic receptor, nicotinic, α polypeptide 10	0.4964	-0.0465	0.1777	-0.0845	0.3789	93 ± 13	97 ± 15	115 ± 10	125 ± 10
207568_at	CHRNA6	cholinergic receptor, nicotinic, α polypeptide 6	0.1486	-0.0233	0.4311	0.4926	0.1019	229 ± 31	234 ± 30	234 ± 20	341 ± 51
210943_s_at	CHS1	Chediak-Higashi syndrome 1	0.5176	-0.0465	0.1558	-0.1652	0.1034	498 ± 37	480 ± 34	496 ± 41	645 ± 77
32094_at	CHST3	carbohydrate sulfotransferase 3	0.0096	-0.0003	-0.1875	-0.3537	0.0133	485 ± 69	513 ± 38	713 ± 91	815 ± 9
221059_s_at	CHST6	carbohydrate sulfotransferase 6	0.0221	-0.0014	0.0043	-0.4750	0.0085	650 ± 50	658 ± 70	926 ± 115	1061 ± 11
201953_at	CIB1	calcium and integrin binding 1	0.0627	-0.0202	0.3059	0.3883	0.0068	721 ± 40	757 ± 48	705 ± 38	942 ± 53
205516_x_at	CIZ1	Cip1-interacting zinc finger protein	0.0077	-0.3116	-0.0616	-0.4456	0.1239	969 ± 85	911 ± 42	1224 ± 87	1043 ± 142
209999_s_at	CKAP4	cytoskeleton-associated protein 4	0.0394	-0.2797	-0.3599	-0.4826	0.3189	539 ± 46	523 ± 42	843 ± 44	604 ± 69
217947_at	CKLFSF6	chemokine-like factor super family 6	0.0564	-0.0011	0.2061	-0.1641	0.0481	644 ± 45	750 ± 54	836 ± 85	944 ± 91
214135_at	CLDN18	claudin 18	0.0326	-0.1671	0.0338	0.4801	0.0680	123 ± 15	187 ± 22	172 ± 17	192 ± 27
204482_at	CLDN5	claudin 5	0.0230	-0.0576	0.0011	-0.3048	0.0121	684 ± 76	1053 ± 123	1262 ± 153	1111 ± 109
221698_s_at	CLECSEF12	C-type lectin, superfamily member 12	0.0650	-0.0036	0.0522	-0.4612	0.0332	225 ± 22	314 ± 44	326 ± 39	415 ± 66
209732_at	CLECSEF2	C-type lectin, superfamily member 2	0.0140	-0.2275	-0.4506	0.4686	0.5504	166 ± 39	204 ± 32	200 ± 35	250 ± 57
208659_at	CLIC1	chloride intracellular channel 1	0.8258	-0.0403	-0.2440	-0.0457	0.4004	486 ± 71	534 ± 50	627 ± 22	614 ± 94
222043_at	CLU	clusterin	0.0230	-0.0176	0.0040	0.0373	0.0226	1111 ± 60	982 ± 60	1716 ± 273	1584 ± 207
61732_l_at	CMG1	capillary morphogenesis protein 1	0.0002	-0.0158	0.0069	-0.0166	0.0255	21 ± 4	31 ± 4	35 ± 5	62 ± 18
201774_s_at	CNAP1	chromosome condensation-related SMC-associated protein 1	0.1620	-0.0075	0.3686	-0.0276	0.2398	147 ± 18	152 ± 31	179 ± 13	202 ± 10
222182_s_at	CNOT2	CCR4-NOT transcription complex, subunit 2	0.0001	-0.0047	-0.2017	0.3698	0.0108	738 ± 65	662 ± 50	1115 ± 104	1163 ± 201
208912_s_at	CNP	2,3'-cyclic nucleotide 3' phosphodiesterase	0.0801	-0.0264	0.1639	-0.4091	0.1319	4700 ± 260	5089 ± 574	6190 ± 593	7447 ± 1806
203073_at	COG2	component of oligomeric golgi complex 2	0.3151	-0.0400	-0.4490	-0.4517	0.1009	703 ± 33	780 ± 66	776 ± 54	883 ± 44
212189_s_at	COG4	component of oligomeric golgi complex 4	0.0419	-0.1525	0.0294	-0.4694	0.1127	335 ± 46	423 ± 42	448 ± 31	486 ± 82
209082_s_at	COL18A1	collagen, type XVIII, α 1	0.0342	-0.0031	-0.1468	-0.4837	0.0165	219 ± 22	265 ± 32	286 ± 18	332 ± 52
202403_s_at	COL1A2	collagen, type I, α 2	0.1289	-0.0035	-0.1983	-0.1062	0.0334	191 ± 20	200 ± 30	197 ± 9	294 ± 32
208096_s_at	COL21A1	collagen, type XXI, α 1	0.0521	-0.0010	-0.4617	-0.4398	0.0069	330 ± 40	348 ± 59	414 ± 77	601 ± 87
222073_at	COL4A3	collagen, type IV, α 3	0.0823	-0.0133	0.3257	-0.2960	0.1181	121 ± 16	126 ± 10	161 ± 20	232 ± 36
213110_s_at	COL4A5	collagen, type IV, α 5	0.3377	-0.0133	0.3257	-0.2960	0.1181	1168 ± 129	1592 ± 264	1661 ± 169	1862 ± 273
209156_s_at	COL6A2	collagen, type VI, α 2	0.0823	-0.0015	-0.2691	-0.4149	0.0233	136 ± 24	134 ± 10	157 ± 28	331 ± 92
201438_at	COL6A3	collagen, type VI, α 3	0.2859	-0.0267	0.2059	0.4789	0.1675	67 ± 12	96 ± 32	153 ± 47	172 ± 43
204136_at	COL7A1	collagen, type VII, α 1	0.0279	-0.1322	0.1597	0.2291	0.2043	197 ± 14	241 ± 73	313 ± 26	310 ± 60
52651_at	COL9A2	collagen, type VIII, α 2	0.0147	-0.0006	0.0083	-0.0204	0.0028	216 ± 20	311 ± 28	317 ± 24	355 ± 24
208817_at	COMT	catechol-O-methyltransferase	0.2906	-0.0093	-0.0950	0.4285	0.0734	644 ± 57	575 ± 42	658 ± 48	853 ± 119
201358_s_at	COPB	coatamer protein complex, subunit β	0.2386	-0.0283	0.0668	-0.1164	0.1351	3174 ± 113	3629 ± 299	3601 ± 165	3994 ± 337
209146_s_at	COQ7	COQ7 coenzyme Q, 7 homolog ubiquinone	0.0231	-0.1475	0.1429	0.2421	0.0726	319 ± 19	358 ± 33	307 ± 27	424 ± 47
214282_at	CP	ceruloplasmin	0.2097	-0.0147	-0.4169	0.3578	0.1093	38 ± 5	39 ± 9	58 ± 9	69 ± 15
206100_at	CPM	carboxypeptidase M	0.1786	-0.0370	0.2926	-0.0122	0.1208	196 ± 25	301 ± 49	301 ± 53	346 ± 44
202118_s_at	CPNE3	copine III	0.0249	-0.0163	0.2366	-0.0141	0.0019	258 ± 28	317 ± 36	424 ± 17	345 ± 23
33132_at	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	0.0495	-0.1760	0.0362	-0.0518	0.0953	483 ± 39	707 ± 77	759 ± 73	713 ± 129
210069_at	CPT1B	caritine palmitoyltransferase I, muscle	0.0011	-0.0028	-0.1709	-0.3727	0.0181	227 ± 24	200 ± 25	301 ± 40	383 ± 65
204264_at	CPT2	caritine palmitoyltransferase II	0.1620	-0.0001	0.0063	-0.0319	0.0017	104 ± 6	133 ± 12	132 ± 13	177 ± 14

Web Table 5 (7)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
217552_x_at	CR1	0.1135	-0.0040	0.3839	-0.0237	0.0830	19 ± 7	35 ± 11	43 ± 13	63 ± 14
205076_s_at	CRA	0.0631	-0.0038	0.4665	-0.3701	0.0619	406 ± 40	398 ± 33	465 ± 36	573 ± 71
209833_at	CRADD	0.0606	-0.0268	-0.3374	-0.4958	0.0583	392 ± 14	371 ± 19	384 ± 14	452 ± 33
209432_s_at	CREB3	0.0020	-0.0104	-0.1206	0.3873	0.0014	708 ± 32	678 ± 31	922 ± 49	831 ± 53
202160_at	CREBBP	0.0002	-0.0116	0.1311	-0.1158	0.0122	1011 ± 56	1138 ± 97	1388 ± 96	1276 ± 76
205984_at	CRHBP	0.0076	-0.0334	-0.3448	-0.4704	0.2320	122 ± 17	128 ± 17	155 ± 26	187 ± 34
219226_at	CRK7	-0.8701	-0.0116	0.4451	-0.4041	0.0483	126 ± 18	106 ± 9	107 ± 10	183 ± 32
206184_at	CRKL	0.2573	-0.0417	-0.4839	-0.1358	0.0794	228 ± 19	260 ± 20	237 ± 21	312 ± 32
206315_at	CSF1	0.1669	-0.0156	0.2908	-0.4871	0.1171	136 ± 41	92 ± 32	240 ± 72	270 ± 59
209716_at	CSK	0.2485	-0.0008	0.1086	-0.0167	0.0039	367 ± 39	506 ± 50	500 ± 44	722 ± 98
202329_at	CSNK1A1	0.0014	-0.0100	0.0856	-0.0762	0.0362	526 ± 46	614 ± 38	799 ± 62	850 ± 48
208865_at	CSNK1E	0.3689	0.0000	-0.1906	-0.1298	0.0125	2970 ± 138	2918 ± 50	3518 ± 81	3846 ± 40
202332_at	CSNK2A2	0.0067	-0.0027	0.3337	0.0660	0.0054	570 ± 58	503 ± 33	746 ± 83	1068 ± 83
203575_at	CSNK2G2	0.0004	-0.0530	0.0046	-0.1334	0.0685	370 ± 8	389 ± 13	459 ± 37	437 ± 31
204619_s_at	CSPG2	0.1038	-0.0247	0.0746	-0.0042	0.1689	389 ± 31	519 ± 63	575 ± 85	558 ± 63
207030_s_at	CSR2	0.0026	-0.0037	-0.1732	-0.2394	0.0369	391 ± 42	381 ± 78	446 ± 45	660 ± 112
205670_at	CST	0.0216	-0.0079	0.0935	-0.1898	0.1771	85 ± 27	145 ± 60	105 ± 23	240 ± 86
20957_at	CTAGE-1	0.3922	-0.0278	0.3270	-0.2087	0.0796	126 ± 14	136 ± 25	129 ± 13	207 ± 40
213980_s_at	CTBP1	0.0411	-0.3020	-0.3468	-0.4501	0.0442	2235 ± 150	1972 ± 57	2554 ± 137	2284 ± 115
210835_s_at	CTBP2	0.0001	-0.0270	0.2167	0.2175	0.0381	2070 ± 200	2304 ± 324	2897 ± 281	3192 ± 374
218923_at	CTBS	0.0282	-0.0332	0.1312	-0.0678	0.0832	207 ± 22	264 ± 22	333 ± 56	315 ± 38
210844_x_at	CTNNA1	0.4535	-0.0044	-0.1227	-0.1602	0.1983	1553 ± 152	1572 ± 212	1888 ± 193	2026 ± 167
221021_s_at	CTNBL1	0.2123	-0.0093	0.1529	-0.1693	0.0256	283 ± 24	353 ± 25	359 ± 12	392 ± 34
36566_at	CTNS	0.0432	-0.0324	0.1469	-0.3789	0.0759	284 ± 35	323 ± 40	334 ± 13	422 ± 51
219080_s_at	CTPS2	0.1321	-0.0001	0.0362	-0.2678	0.0003	93 ± 11	112 ± 11	109 ± 13	196 ± 24
205297_at	CTRC	0.3537	-0.0247	0.0352	-0.4192	0.0299	162 ± 22	195 ± 30	181 ± 29	293 ± 43
214377_s_at	CTRL	0.0081	-0.1180	-0.1313	0.4411	0.2503	208 ± 24	220 ± 28	226 ± 15	285 ± 42
213275_x_at	CTSB	0.0307	-0.0190	0.2080	-0.3207	0.0729	3611 ± 346	3316 ± 265	3940 ± 318	5016 ± 695
202295_s_at	CTSH	0.1658	-0.0362	-0.4007	-0.0755	0.3380	1821 ± 234	1787 ± 351	2375 ± 324	2354 ± 294
202087_s_at	CTSL	0.5555	-0.0272	-0.4994	-0.0402	0.6177	647 ± 40	679 ± 62	733 ± 60	743 ± 80
202901_x_at	CTSS	0.4358	-0.0489	0.0065	-0.0708	0.1185	95 ± 8	144 ± 18	134 ± 18	149 ± 22
201424_s_at	CUL4A	0.0518	-0.0168	0.2723	-0.0061	0.0353	336 ± 21	386 ± 43	483 ± 46	441 ± 28
203533_s_at	CUL5	0.1935	-0.0367	-0.1648	-0.0905	0.0401	225 ± 19	188 ± 27	266 ± 13	254 ± 16
214743_at	CUTL1	0.0013	-0.0014	0.2620	0.0981	0.0042	801 ± 35	714 ± 86	943 ± 81	1255 ± 154
209774_x_at	CXCL2	0.1268	-0.0015	-0.3813	-0.3027	0.0389	120 ± 15	146 ± 21	199 ± 31	209 ± 24
213681_at	CYHR1	0.0110	-0.0373	-0.1514	-0.0675	0.1174	204 ± 22	220 ± 18	207 ± 17	285 ± 39
216809_at	CYLC1	0.0074	0.0000	0.1655	-0.1105	0.0001	106 ± 11	128 ± 15	151 ± 10	239 ± 29
211031_s_at	CYLN2	0.0373	-0.1178	0.3550	-0.1301	0.0262	1267 ± 154	1318 ± 90	1908 ± 142	1380 ± 229
204309_at	CYP11A	0.1618	-0.0057	0.2687	-0.0285	0.0499	119 ± 12	143 ± 6	150 ± 6	175 ± 23
217558_at	CYP2C9	0.0985	-0.0008	0.1531	-0.4189	0.0084	78 ± 11	76 ± 5	93 ± 13	144 ± 21
220432_s_at	CYP3A1	0.0859	-0.0161	0.0101	-0.1890	0.1592	31 ± 5	40 ± 9	45 ± 5	57 ± 12
205998_x_at	CYP3A4	0.0692	-0.0135	0.2344	-0.3041	0.0389	605 ± 28	722 ± 91	711 ± 44	868 ± 68

Web Table 5 (8)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
206515_at	CYP4F3	cytochrome P450, subfamily 1F, polypeptide 3	0.0923	-0.0010	0.0076	-0.3227	0.0230	124 ± 17	143 ± 30	229 ± 52	367 ± 94
204190_at	D13S106E	highly charged protein	0.0166	-0.2346	-0.1781	0.2969	0.2799	551 ± 44	567 ± 45	522 ± 43	688 ± 105
202646_s_at	D1S155E	NRAS-related gene	0.0484	-0.1550	0.0010	-0.1643	0.3444	2687 ± 151	2897 ± 196	3029 ± 101	2993 ± 141
216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	0.0015	-0.1112	0.2206	0.2471	0.0891	839 ± 26	824 ± 50	1042 ± 111	904 ± 15
212793_at	DAAM2	dishevelled associated activator of morphogenesis 2	0.0038	-0.0114	0.1578	-0.0982	0.0608	3452 ± 394	4531 ± 634	5302 ± 359	5565 ± 939
205417_s_at	DAG1	dystroglycan 1	0.1294	-0.0107	0.2535	-0.4654	0.0828	1326 ± 94	1328 ± 86	1592 ± 102	1639 ± 148
208878_at	DAO	D-amino-acid oxidase	0.2293	-0.0445	0.0137	-0.3370	0.0862	270 ± 15	335 ± 60	321 ± 32	432 ± 50
206324_s_at	DAPK2	death-associated protein kinase 2	0.0267	-0.0082	0.0843	-0.0030	0.0044	122 ± 15	174 ± 16	141 ± 7	265 ± 50
203891_s_at	DAPK3	death-associated protein kinase 3	0.0397	-0.0080	0.0604	-0.4720	0.0043	100 ± 10	139 ± 21	134 ± 9	214 ± 33
201623_s_at	DARS	aspartyl-tRNA synthetase	0.6838	-0.0082	0.0183	-0.0978	0.1298	1240 ± 48	1426 ± 57	1476 ± 115	1625 ± 181
208281_x_at	DAZ3	deleted in azoospermia 3	0.5587	-0.0330	0.3063	-0.2133	0.1894	111 ± 13	126 ± 13	129 ± 15	166 ± 16
218443_s_at	DAZAP1	DAZ associated protein 1	0.0020	-0.0492	0.1234	0.3117	0.1403	439 ± 32	505 ± 53	523 ± 35	598 ± 70
214334_x_at	DAZAP2	DAZ associated protein 2	0.4612	-0.0221	-0.4577	-0.4672	0.1398	4825 ± 241	5432 ± 532	5819 ± 442	6184 ± 491
201678_s_at	DC12	DC12 protein	0.0959	-0.0222	-0.1699	-0.4385	0.0528	541 ± 49	490 ± 40	533 ± 40	674 ± 45
20759_s_at	DCI	dodecyl-Coenzyme A 5 isomerase	0.0751	-0.0024	0.2597	-0.4718	0.0158	303 ± 27	310 ± 50	338 ± 23	493 ± 66
219678_x_at	DCLRE1C	DNA cross-link repair 1C	0.0015	-0.0240	0.3760	-0.4335	0.1549	658 ± 71	694 ± 84	955 ± 161	993 ± 171
209335_at	DCN	decorin	0.6224	-0.0495	0.4554	-0.0316	0.3997	246 ± 17	292 ± 13	282 ± 28	317 ± 47
208779_x_at	DDR1	discoidin domain receptor family, member 1	0.0030	-0.0014	0.2272	-0.1356	0.0103	2859 ± 317	3596 ± 440	4527 ± 383	4669 ± 516
205168_at	DDR2	discoidin domain receptor family, member 2	0.0177	-0.0001	0.0891	-0.1388	0.0017	295 ± 53	323 ± 32	471 ± 51	773 ± 145
208895_s_at	DDX18	DEAD/H box polypeptide 18	0.0017	-0.1057	-0.3871	0.4609	0.1582	1132 ± 90	1086 ± 73	1076 ± 99	1460 ± 223
208152_s_at	DDX21	DEAD/H box polypeptide 21	0.4080	-0.0177	0.4509	0.4093	0.0318	885 ± 53	943 ± 101	828 ± 32	1192 ± 130
215693_x_at	DDX27	DEAD/H box polypeptide 27	0.0022	-0.0129	-0.2769	-0.4938	0.0625	857 ± 64	878 ± 80	937 ± 56	1121 ± 85
201584_s_at	DDX39	DEAD/H box polypeptide 39	0.0009	-0.0061	0.3404	-0.4461	0.0148	585 ± 43	730 ± 89	749 ± 47	971 ± 114
204909_at	DDX6	DEAD/H box polypeptide 6	0.0213	-0.0113	0.1479	-0.1763	0.0629	184 ± 27	163 ± 21	241 ± 21	298 ± 60
207269_at	DEFA4	defensin, α4, corticostatin	0.1017	-0.0383	0.3230	0.3105	0.0133	121 ± 17	93 ± 10	114 ± 14	192 ± 32
208024_s_at	DGCR6	DiGeorge syndrome critical region gene 6	0.0406	-0.7078	0.0413	-0.1414	0.0739	771 ± 56	849 ± 30	1027 ± 59	835 ± 113
206395_at	DGKG	diacylglycerol kinase, γ 90kDa	0.0084	-0.0392	-0.4413	-0.2059	0.0488	415 ± 25	441 ± 37	550 ± 62	632 ± 95
204383_at	DGSI	DiGeorge syndrome critical region gene DGSI	0.0490	-0.0081	0.0315	-0.1106	0.0821	276 ± 16	273 ± 19	319 ± 22	364 ± 43
202534_x_at	DHFR	dihydrofolate reductase	0.1505	-0.0174	0.0503	0.3447	0.0405	546 ± 25	644 ± 95	733 ± 71	810 ± 64
213632_at	DHODH	dihydroorotate dehydrogenase	0.1321	-0.0017	-0.3591	0.4442	0.0095	152 ± 16	139 ± 13	153 ± 9	252 ± 44
205603_s_at	DIAPH2	diaphanous homolog 2	0.0285	-0.0631	0.1489	0.2158	0.0581	163 ± 17	213 ± 49	267 ± 20	273 ± 41
206061_s_at	DICER1	Dicer1, Dcr-1 homolog	0.1312	-0.0282	0.4132	-0.0319	0.1687	469 ± 33	533 ± 77	596 ± 59	637 ± 55
215529_x_at	DIP2	disco-interacting protein 2 homolog	0.0041	-0.1117	0.1679	-0.0180	0.4337	600 ± 77	753 ± 83	844 ± 170	923 ± 226
214274_s_at	DLEC1	deleted in lung and esophageal cancer 1	0.0222	-0.2592	0.2302	0.2129	0.3234	891 ± 39	971 ± 86	1061 ± 63	1033 ± 88
205677_s_at	DLEU1	deleted in lymphocytic leukemia, 1	0.3159	-0.0123	0.4122	0.4914	0.0961	271 ± 25	302 ± 36	306 ± 18	384 ± 42
201681_s_at	DLG5	discs, large homolog 5	0.0001	-0.0012	-0.0242	0.2884	0.0057	459 ± 43	493 ± 67	689 ± 62	718 ± 63
208216_at	DLX4	distal-less homeobox 4	0.1211	-0.0191	0.0476	-0.0376	0.0790	118 ± 14	138 ± 11	154 ± 21	194 ± 30
208382_s_at	DMC1	DMC1 dosage suppressor of mek1 homolog	0.2943	-0.0442	0.0145	-0.0010	0.0125	121 ± 6	187 ± 24	132 ± 16	219 ± 34
212730_at	DMN	desmulin	0.0011	-0.0008	-0.0045	-0.4739	0.0005	2024 ± 230	1812 ± 243	3472 ± 380	3170 ± 269
37996_s_at	DMPK	dystrophin myotonic-protein kinase	0.0096	-0.0077	-0.4543	0.2331	0.0150	515 ± 33	459 ± 49	621 ± 38	758 ± 109
33768_at	DMWD	dystrophin myotonic-containing WD repeat motif	0.0464	-0.0080	-0.4711	0.3340	0.0430	1105 ± 72	1202 ± 128	1491 ± 125	1560 ± 177
202500_at	DNAJB2	DnaJ homolog, subfamily B, member 2	0.0000	-0.0820	-0.1415	-0.3158	0.2546	1044 ± 126	1000 ± 134	1484 ± 188	1612 ± 479

Web Table 5 (9)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
206782_s_at	DnaJ homolog, subfamily C, member 4	0.1528	-0.0496	0.3372	0.1169	0.0948	237 ± 15	223 ± 31	242 ± 10	314 ± 42
221677_s_at	downstream neighbor of SON	0.2701	-0.0462	-0.0867	-0.4673	0.1337	270 ± 31	269 ± 29	270 ± 18	348 ± 24
220483_s_at	double ring-finger protein, Dornfin	0.0000	-0.0462	0.1766	0.4139	0.0131	85 ± 10	103 ± 22	151 ± 21	168 ± 25
222041_at	diphtheria toxin resistance protein	0.0901	-0.0076	0.2567	0.4324	0.0406	284 ± 20	289 ± 26	322 ± 24	382 ± 30
21431_s_at	dihydropyrimidinase-like 3	0.1273	-0.0169	0.1126	-0.3099	0.0408	1944 ± 171	1972 ± 138	3087 ± 420	2680 ± 414
206590_x_at	dopamine receptor D2	0.0231	-0.0193	-0.2246	-0.4492	0.0327	250 ± 26	251 ± 9	273 ± 20	358 ± 44
206032_at	desmocollin 3	0.0338	-0.0466	0.2311	0.1407	0.0591	105 ± 18	102 ± 14	133 ± 11	191 ± 43
200606_at	desmoplakin	0.3852	-0.0076	0.2251	0.3171	0.0227	157 ± 16	189 ± 21	286 ± 38	347 ± 81
205741_s_at	dystrobrein, α	0.0794	-0.0375	-0.1328	-0.2852	0.2491	781 ± 138	714 ± 106	934 ± 162	1260 ± 331
38037_at	diphtheria toxin receptor	0.0040	0.0000	-0.2801	0.3925	0.0002	200 ± 16	195 ± 20	228 ± 19	329 ± 25
205777_at	dual specificity phosphatase 9	0.0234	-0.0209	-0.1090	0.2903	0.0348	273 ± 38	223 ± 21	322 ± 32	409 ± 60
208955_at	dUTP pyrophosphatase	0.2888	-0.0354	-0.2468	0.3855	0.0106	309 ± 24	309 ± 16	300 ± 9	404 ± 34
222247_at	putative X-linked retinopathy protein	0.4498	-0.0042	0.1001	-0.0160	0.0358	117 ± 8	141 ± 15	147 ± 13	175 ± 17
203262_s_at	DNA segment on chromosome X 9928 expressed sequence	0.0101	-0.0060	-0.1346	0.3718	0.0316	882 ± 87	929 ± 92	987 ± 52	1250 ± 113
208713_at	E1B-55kDa-associated protein 5	0.0926	-0.0300	0.0236	-0.2869	0.0231	611 ± 39	810 ± 73	758 ± 39	833 ± 67
222051_s_at	E2F transcription factor 5, p130-binding	0.0540	-0.0236	0.3119	-0.4168	0.0105	81 ± 12	121 ± 28	91 ± 10	219 ± 55
201749_at	endothelin converting enzyme 1	0.0323	-0.0025	0.4218	-0.1976	0.0488	367 ± 65	371 ± 39	524 ± 53	660 ± 31
217497_at	endothelial cell growth factor 1	0.0970	-0.0138	0.1474	-0.2875	0.0452	106 ± 18	76 ± 12	109 ± 19	158 ± 19
206101_at	extracellular matrix protein 2	0.0530	-0.0115	0.1719	-0.1344	0.0308	249 ± 29	301 ± 44	493 ± 112	471 ± 48
220048_at	ectodysplasin 1, anhidrotic receptor	0.0458	-0.0953	0.1863	0.1967	0.0539	270 ± 26	305 ± 62	268 ± 14	417 ± 48
209058_at	endothelial differentiation-related factor 1	0.0272	-0.0463	0.1657	0.1372	0.0451	1566 ± 70	1531 ± 71	1730 ± 205	1798 ± 251
204464_s_at	endothelin receptor type A	0.0209	-0.1151	0.0798	-0.0423	0.4552	178 ± 16	211 ± 21	217 ± 22	229 ± 33
200919_at	early development regulator 2	0.4775	-0.0291	0.2193	0.4029	0.0627	1650 ± 93	1859 ± 107	1756 ± 85	2114 ± 182
213614_x_at	eukaryotic translation elongation factor 1 α 1	0.0016	-0.0986	0.4804	0.1604	0.0275	16900 ± 813	16222 ± 317	1548 ± 1268	9010 ± 1956
203113_s_at	eukaryotic translation elongation factor 1 δ	0.0083	-0.2413	-0.2392	0.3612	0.4500	2217 ± 280	2326 ± 314	2813 ± 234	2750 ± 448
200689_x_at	eukaryotic translation elongation factor 1 γ	0.0189	-0.5812	0.1266	-0.2644	0.1342	6523 ± 381	7297 ± 471	8204 ± 669	6937 ± 528
201843_s_at	EGF-containing fibulin-like extracellular matrix protein 1	0.1235	-0.0248	0.2269	-0.0413	0.2709	518 ± 50	673 ± 145	812 ± 189	935 ± 191
206580_s_at	EGF-containing fibulin-like extracellular matrix protein 2	0.0049	-0.0071	0.0496	-0.0812	0.0171	682 ± 79	701 ± 61	1081 ± 90	1051 ± 173
202023_at	ephrin-A1	0.0080	-0.0304	-0.0845	-0.3531	0.1948	334 ± 51	325 ± 57	468 ± 65	517 ± 115
204400_at	signal transduction protein	0.0025	-0.0284	0.0723	-0.2872	0.1001	575 ± 52	765 ± 115	806 ± 79	1099 ± 275
206254_at	epidermal growth factor	0.0576	-0.0481	-0.3784	-0.4958	0.0743	84 ± 7	98 ± 15	86 ± 21	156 ± 35
211551_at	epidermal growth factor receptor	0.2659	-0.0047	0.2270	-0.1849	0.0266	235 ± 24	255 ± 16	284 ± 19	342 ± 32
220956_s_at	egl nine homolog 2	0.0983	-0.0276	0.2139	-0.1987	0.2456	622 ± 54	591 ± 55	649 ± 31	739 ± 55
208112_x_at	EH-domain containing 1	0.0002	0.0000	0.2233	-0.0891	0.0000	264 ± 33	348 ± 29	453 ± 37	609 ± 61
212351_at	eukaryotic translation initiation factor 2B, subunit 5 epsilon	0.0149	-0.0731	-0.0084	-0.2207	0.2530	423 ± 18	398 ± 29	437 ± 31	485 ± 38
218287_s_at	eukaryotic translation initiation factor 2C, 1	0.0175	-0.1229	0.0238	-0.4644	0.1303	476 ± 30	586 ± 56	592 ± 30	663 ± 89
203462_x_at	eukaryotic translation initiation factor 3, subunit 9 alpha	0.0066	-0.0008	-0.4073	0.4087	0.0073	1209 ± 43	1209 ± 83	1354 ± 57	1521 ± 74
211937_at	eukaryotic translation initiation factor 4B	0.0003	-0.0967	0.0971	0.3661	0.1363	1205 ± 67	1275 ± 176	1680 ± 136	1506 ± 208
208707_at	eukaryotic translation initiation factor 5	0.0526	-0.0043	0.1410	-0.2343	0.0386	549 ± 24	568 ± 40	648 ± 50	695 ± 36
219325_s_at	elaC homolog 1	0.0252	-0.0430	0.0639	0.4195	0.0400	48 ± 8	66 ± 17	66 ± 5	98 ± 14
203822_s_at	E74-like factor 2	0.2468	-0.0281	-0.3003	-0.4960	0.0337	774 ± 47	849 ± 77	748 ± 41	1010 ± 83
31845_at	E74-like factor 4	0.1010	-0.0203	0.2169	0.3826	0.0539	97 ± 14	126 ± 27	112 ± 10	182 ± 34

Web Table 5 (10)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
203617_x_at	ELK1	ELK1, member of ETS oncogene family	0.0366	-0.1253	0.3243	0.4405	0.2507	1084 ± 116	1339 ± 214	1423 ± 72	1547 ± 242
220366_at	ELSPBP1	epididymal sperm binding protein 1	0.0329	-0.0602	0.1542	0.4590	0.1215	153 ± 17	186 ± 31	183 ± 16	259 ± 53
204398_s_at	EML2	echinoderm microtubule associated protein like 2	0.0821	-0.0482	0.3391	-0.3220	0.0842	591 ± 60	662 ± 57	591 ± 33	819 ± 108
201324_at	EMP1	epithelial membrane protein 1	0.0170	-0.0010	-0.3348	-0.0792	0.0249	232 ± 41	216 ± 45	347 ± 46	501 ± 117
217820_s_at	ENAH	enabled homolog	0.0499	-0.0125	0.2796	-0.0357	0.0402	1003 ± 42	1081 ± 99	1448 ± 189	1346 ± 61
37408_at	ENDO180	endocytic receptor	0.0634	-0.0157	0.0815	-0.0639	0.0048	436 ± 41	509 ± 23	384 ± 28	751 ± 27
213579_s_at	EP300	E1A binding protein p300	0.0097	-0.0009	0.1249	-0.0004	0.0051	203 ± 25	266 ± 19	246 ± 21	348 ± 36
212376_s_at	EP400	E1A binding protein p400	0.0074	-0.0020	0.0508	0.4744	0.2432	371 ± 17	379 ± 16	445 ± 18	421 ± 53
201061_s_at	EPB72	erythrocyte membrane protein band 7.2	0.0032	-0.0070	0.3088	-0.3868	0.0282	2615 ± 197	2692 ± 271	3102 ± 203	3571 ± 263
37986_at	EPOR	erythropoietin receptor	0.0274	-0.2770	0.0608	-0.3140	0.0129	223 ± 21	210 ± 33	216 ± 10	343 ± 47
200842_s_at	EPRS	glutaryl-prolyl-HRNA synthetase	0.0067	-0.0694	-0.4863	-0.1668	0.1271	594 ± 52	576 ± 58	682 ± 75	844 ± 135
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	0.4848	-0.0113	0.3343	-0.0202	0.3262	813 ± 39	849 ± 102	1025 ± 88	1024 ± 171
212087_s_at	ERAL1	Era G-protein-like 1	0.2567	-0.0210	0.0372	-0.0020	0.0745	589 ± 26	656 ± 33	633 ± 55	783 ± 76
217941_s_at	ERBB2IP	erbB2 interacting protein	0.0126	-0.0033	-0.4232	-0.0457	0.0032	2624 ± 324	3068 ± 269	4899 ± 635	4093 ± 386
206794_at	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	0.0094	-0.5273	0.1832	-0.2239	0.7749	86 ± 11	97 ± 11	97 ± 9	106 ± 25
207347_at	ERCC6	excision repair cross-complementing group 6	0.0610	-0.0303	0.1977	-0.3328	0.0963	225 ± 23	227 ± 17	247 ± 23	326 ± 50
203643_at	ERF	Ets2 repressor factor	0.0078	-0.0039	0.0463	-0.1209	0.0003	181 ± 32	363 ± 33	447 ± 52	420 ± 48
208958_at	ERp44	endoplasmic reticulum resident protein 44 kDa	0.6145	-0.0404	0.1841	-0.0993	0.0730	154 ± 11	150 ± 9	213 ± 22	188 ± 24
208658_at	ERP70	protein disulfide isomerase related protein	0.0124	-0.0576	-0.3718	0.4224	0.3098	369 ± 40	361 ± 45	413 ± 37	485 ± 74
213873_at	ESDN	endothelial & sm. muscle cell-derived neuropilin-like protein	0.0565	-0.0356	0.0192	-0.1737	0.1039	152 ± 10	205 ± 20	195 ± 16	256 ± 53
202081_at	ETR101	immediate early protein	0.2720	-0.0060	-0.2287	0.2698	0.0254	1192 ± 82	1165 ± 157	1286 ± 107	1676 ± 141
204774_at	EV12A	ectotropic viral integration site 2A	0.6624	-0.0052	0.2425	-0.3038	0.2040	1650 ± 156	1820 ± 291	2110 ± 241	2297 ± 237
211742_s_at	EV12B	ectotropic viral integration site 2B	0.5752	-0.0168	0.3591	-0.0897	0.2783	438 ± 56	486 ± 57	508 ± 40	578 ± 42
209214_s_at	EWSR1	Ewing sarcoma breakpoint region 1	0.0184	-0.0016	0.3634	-0.0204	0.0163	1151 ± 47	1317 ± 96	1371 ± 42	1466 ± 69
50376_at	EZF-2	endothelial zinc finger protein 2	0.0047	-0.0929	0.0357	-0.4982	0.0750	943 ± 78	1307 ± 234	1181 ± 136	1619 ± 229
203989_x_at	F2R	coagulation factor II receptor	0.2415	-0.0155	0.0442	-0.0761	0.0227	49 ± 8	67 ± 7	63 ± 10	100 ± 18
219429_at	FAAH	fatty acid hydroxylase	0.7656	-0.0105	0.4165	-0.4211	0.1621	1173 ± 105	1066 ± 129	1304 ± 156	1625 ± 264
201963_at	FACL2	fatty acid-Coenzyme A ligase, long-chain 2	0.9855	-0.0127	-0.1234	-0.2482	0.1972	1446 ± 132	1425 ± 189	1375 ± 132	1975 ± 350
208962_s_at	FADS1	fatty acid desaturase 1	0.0077	-0.0010	0.0692	-0.0475	0.0059	1176 ± 114	1536 ± 158	2085 ± 232	2454 ± 398
204257_at	FADS3	fatty acid desaturase 3	0.0517	-0.0355	0.4612	0.1031	0.1085	490 ± 26	472 ± 25	499 ± 40	629 ± 78
209405_s_at	FAM3A	fatty acid desaturase 3	0.0042	-0.2095	0.0299	0.2812	0.1813	267 ± 9	341 ± 45	397 ± 54	369 ± 52
220255_at	FANCE	family with sequence similarity 3, member A	0.0172	-0.0410	-0.4864	-0.1755	0.1587	106 ± 13	95 ± 24	123 ± 12	155 ± 21
202995_s_at	FBLN1	Fanconi anemia, complementation group E	0.0296	-0.1146	0.3952	0.2100	0.2188	190 ± 15	188 ± 17	200 ± 16	272 ± 59
202766_s_at	FBN1	fibrillin 1	0.0393	-0.0008	-0.3708	-0.0354	0.0410	303 ± 25	313 ± 18	385 ± 24	395 ± 39
203184_at	FBN2	fibrillin 2	0.0038	-0.0005	0.0026	-0.1568	0.0004	73 ± 8	100 ± 4	95 ± 10	156 ± 21
213940_s_at	FBP17	fornin-binding protein 17	0.0310	-0.2360	0.0361	-0.1219	0.0597	266 ± 35	377 ± 65	485 ± 71	346 ± 52
208988_at	FBXL11	F-box and leucine-rich repeat protein 11	0.0420	-0.3816	-0.3414	-0.2992	0.4891	917 ± 80	790 ± 31	959 ± 52	941 ± 111
209005_at	FBXL5	F-box and leucine-rich repeat protein 5	0.0149	-0.1215	0.4708	0.3412	0.3649	1150 ± 68	1165 ± 102	1220 ± 61	1339 ± 90
213249_at	FBXL7	F-box and leucine-rich repeat protein 7	0.0883	-0.0007	0.4879	-0.2287	0.0496	580 ± 50	623 ± 32	719 ± 42	774 ± 74
219305_x_at	FBXO2	F-box only protein 2	0.1118	-0.0089	-0.4853	-0.1051	0.1061	1464 ± 100	1512 ± 186	1764 ± 156	2076 ± 273
212991_at	FBXO9	F-box only protein 9	0.0175	-0.0685	-0.3605	-0.3832	0.1810	534 ± 53	464 ± 29	675 ± 76	814 ± 207
214623_at	FBXW3	F-box and WD-40 domain protein 3	0.0084	-0.0163	0.0019	-0.0990	0.0179	34 ± 9	69 ± 18	80 ± 18	134 ± 35

Web Table 5 (11)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
208647_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	0.1174	-0.0001	-0.0372	-0.3202	0.0044	3066 ± 241	2739 ± 279	3693 ± 128	4054 ± 317
201275_at	FDPS	farnesyl diphosphate synthase	0.1716	-0.0040	-0.2270	-0.2568	0.0348	495 ± 36	491 ± 41	623 ± 47	646 ± 52
37384_at	FEM-2	partner of PIX 2	0.0099	-0.0029	-0.0720	0.2527	0.0063	601 ± 49	481 ± 38	687 ± 45	818 ± 90
214417_s_at	FETUB	fetuin B	0.0390	-0.0034	0.0538	-0.2644	0.0002	74 ± 7	111 ± 9	95 ± 9	152 ± 18
203562_at	FEZ1	fasciculation and elongation protein zeta 1	0.1361	-0.0112	0.0477	0.4564	0.1458	8620 ± 513	3094 ± 1000	9994 ± 861	11074 ± 716
210704_at	FEZ2	fasciculation and elongation protein zeta 2	0.0306	-0.0594	0.2365	0.3726	0.0849	125 ± 10	157 ± 16	148 ± 15	194 ± 30
205117_at	FGF1	fibroblast growth factor 1	0.0335	-0.0466	0.3218	-0.2871	0.1717	2890 ± 414	3520 ± 567	4195 ± 455	4073 ± 418
214284_s_at	FGF18	fibroblast growth factor 18	0.0350	-0.2066	0.1269	-0.4345	0.1048	79 ± 10	78 ± 11	130 ± 18	105 ± 25
211535_s_at	FGFR1	fibroblast growth factor receptor 1	0.0308	-0.0134	-0.3851	-0.0706	0.1287	553 ± 44	624 ± 78	706 ± 85	776 ± 164
214379_s_at	FGFR3	fibroblast growth factor receptor 3	0.0009	-0.0075	0.0018	-0.1005	0.0349	1925 ± 183	2388 ± 291	3023 ± 414	3684 ± 478
205305_at	FGL1	fibronogen-like 1	0.0010	-0.0038	0.2055	-0.0102	0.0214	158 ± 14	189 ± 13	223 ± 23	266 ± 50
203734_at	FOX	FOXJ2 forkhead factor	0.0165	-0.0008	0.0703	-0.1768	0.0004	538 ± 24	628 ± 47	556 ± 30	832 ± 7
40850_at	FKBP8	FK506 binding protein 8, 38kDa	0.0214	-0.8156	-0.3324	-0.3505	0.1388	789 ± 109	959 ± 155	1328 ± 141	871 ± 276
222065_s_at	FLII	flightless I homolog	0.0534	-0.0288	-0.4035	-0.0297	0.2726	324 ± 17	359 ± 46	386 ± 10	365 ± 31
218993_at	FLJ10581	putative RNA methyltransferase	0.0125	-0.1307	0.1828	-0.0363	0.0507	348 ± 13	364 ± 13	329 ± 30	430 ± 36
218485_s_at	FLJ11320	GDP-fucose transporter 1	0.1421	-0.0224	0.1217	-0.0303	0.0163	182 ± 15	202 ± 12	180 ± 17	270 ± 33
218658_s_at	FLJ12934	likely ortholog of mouse actin-related protein 8 homolog	0.0081	-0.0206	0.0037	-0.1453	0.0018	205 ± 13	313 ± 38	300 ± 7	330 ± 21
208919_s_at	FLJ13052	NAD kinase	0.1013	-0.0038	-0.2803	0.1632	0.0083	637 ± 23	640 ± 45	798 ± 37	823 ± 69
219020_at	FLJ14249	hypothetical protein FLJ14249 similar to HS1 binding protein 3	0.0129	-0.0078	0.1252	0.4713	0.0262	572 ± 40	666 ± 72	645 ± 27	840 ± 93
220349_s_at	FLJ21865	endo-β-N-acetylglucosaminidase	0.0002	-0.0027	0.4989	-0.2325	0.0199	290 ± 28	307 ± 34	353 ± 50	515 ± 84
219677_at	FLJ22393	SPRY domain-containing SOCS box protein SSB-1	0.0150	-0.1910	0.2423	0.4844	0.2943	271 ± 33	347 ± 60	337 ± 25	406 ± 76
220078_at	FLJ23277	FLJ23277 protein	0.0286	-0.0037	0.2386	-0.0590	0.0332	153 ± 22	197 ± 23	218 ± 14	265 ± 34
214752_x_at	FLNA	filamin A, α	0.0016	-0.0016	0.0618	0.3999	0.0197	375 ± 32	376 ± 33	504 ± 52	631 ± 103
207876_s_at	FLNC	filamin C, γ	0.0000	-0.0031	0.0096	-0.2264	0.0220	296 ± 28	363 ± 88	487 ± 52	576 ± 90
211726_s_at	FMO2	flavin containing monooxygenase 2	0.0111	-0.0001	0.1205	-0.2048	0.0038	213 ± 17	221 ± 11	313 ± 27	371 ± 52
218053_at	FNBP3	formin binding protein 3	0.0032	-0.0028	0.0247	-0.0094	0.0012	820 ± 51	979 ± 63	1334 ± 126	1194 ± 80
211303_x_at	FOLH1	folate hydrolase 1	0.5866	-0.0116	0.4028	-0.0704	0.0734	209 ± 15	182 ± 33	319 ± 66	389 ± 88
202724_s_at	FOXO1A	forkhead box O1A	0.0008	0.0000	0.3251	-0.1806	0.0002	429 ± 27	514 ± 47	638 ± 44	745 ± 56
204131_s_at	FOXO3A	forkhead box O3A	0.0016	-0.0039	0.2351	-0.2294	0.0246	1779 ± 163	1890 ± 150	2030 ± 170	2696 ± 329
219889_at	FRAT1	frequently rearranged in advanced T-cell lymphomas	0.0287	-0.0351	0.1516	0.3567	0.0079	253 ± 17	290 ± 35	269 ± 15	387 ± 36
203592_s_at	FSTL3	folistatin-like 3	0.0135	-0.0880	-0.1028	0.3068	0.1070	342 ± 33	340 ± 38	331 ± 31	517 ± 107
214211_at	FTH1	ferritin, heavy polypeptide 1	0.0031	-0.0120	0.0583	-0.2873	0.0508	5115 ± 224	5411 ± 567	6197 ± 500	6658 ± 227
220856_x_at	FTL	ferritin, light polypeptide	0.0025	-0.0411	0.0107	-0.3321	0.0771	150 ± 8	165 ± 12	164 ± 13	209 ± 27
210808_s_at	FUT2	fucoyltransferase 2	0.0037	-0.0255	0.2682	-0.0355	0.1621	1159 ± 84	1279 ± 108	1477 ± 108	1416 ± 139
202419_at	FVT1	follicular lymphoma variant translocation 1	0.0053	-0.2314	-0.4560	-0.3281	0.4178	339 ± 36	349 ± 38	322 ± 39	468 ± 125
201635_s_at	FXR1	fragile X mental retardation, autosomal homolog 1	0.0017	-0.0002	-0.3794	-0.2551	0.0004	189 ± 24	190 ± 11	214 ± 22	338 ± 30
218204_s_at	FYCO1	FYVE and coiled-coil domain containing 1	0.1121	-0.0214	0.2110	-0.0053	0.0766	729 ± 44	807 ± 99	1057 ± 118	954 ± 113
212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.2412	-0.0097	0.0959	-0.2894	0.0755	154 ± 14	174 ± 25	161 ± 11	219 ± 21
219764_at	FZD10	frizzled homolog 10	0.0802	-0.0012	0.0051	-0.0004	0.0042	114 ± 9	162 ± 8	177 ± 15	194 ± 22
209414_at	FZR1	Fzr1 protein	0.0001	-0.1379	0.1634	-0.1570	0.0760	233 ± 17	289 ± 23	355 ± 31	309 ± 57
202275_at	G6PD	glucose-6-phosphate dehydrogenase	0.0202	-0.2032	0.0723	-0.4535	0.4749	1281 ± 77	1465 ± 172	1393 ± 72	1660 ± 308
203853_s_at	GAB2	GRB2-associated binding protein 2									

Web Table 5 (12)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
220886_at	GABRQ	γ-aminobutyric acid receptor, theta	0.1085	-0.0081	0.0039	-0.0036	0.0063	98 ± 11	188 ± 27	155 ± 13	-205 ± 29
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, β	0.4308	-0.0124	-0.2865	-0.2601	0.1684	200 ± 83	252 ± 88	251 ± 57	529 ± 174
204121_at	GADD45G	growth arrest and DNA-damage-inducible, γ	0.0529	-0.0019	-0.2213	-0.3086	0.0079	135 ± 17	140 ± 34	178 ± 18	256 ± 31
207086_x_at	GAGE4	G antigen 4	0.0403	-0.0749	0.2067	-0.3665	0.0374	118 ± 14	138 ± 16	119 ± 9	-213 ± 48
208155_x_at	GAGE6	G antigen 6	0.0492	-0.0148	0.2833	0.2955	0.0531	126 ± 10	127 ± 19	169 ± 12	181 ± 25
40225_at	GAK	cyclin G associated kinase	0.0110	-0.0547	0.4185	0.2943	0.0997	1839 ± 167	1896 ± 349	1959 ± 92	2761 ± 133
201723_s_at	GALNT1	polypeptide N-acetylgalactosaminyltransferase 1	0.3002	-0.0336	0.4142	-0.1813	0.1038	512 ± 23	533 ± 16	585 ± 26	600 ± 43
219956_at	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	0.5226	-0.0081	-0.2252	-0.3535	0.0998	316 ± 33	323 ± 28	361 ± 80	539 ± 87
220929_at	GALNT8	polypeptide N-acetylgalactosaminyltransferase 8	0.0011	-0.0598	-0.2898	0.3891	0.2407	132 ± 12	144 ± 9	163 ± 20	192 ± 37
205354_at	GAMT	guanidinoacetate N-methyltransferase	0.0054	-0.0940	0.0021	-0.1239	0.1569	317 ± 31	370 ± 30	364 ± 43	478 ± 80
204028_s_at	GAPCEN	rab6 GTPase activating protein	0.0039	-0.0231	0.1198	-0.3690	0.0537	1472 ± 78	1620 ± 85	1747 ± 129	1902 ± 121
208138_at	GAS	gastrin	0.6262	-0.0311	0.1528	-0.1679	0.0704	223 ± 24	270 ± 29	240 ± 22	327 ± 31
204457_s_at	GAS1	growth arrest-specific 1	0.0047	-0.0060	-0.1530	-0.2460	0.0807	331 ± 37	349 ± 63	390 ± 66	526 ± 5
31874_at	GASZL1	growth arrest-specific 2 like 1	0.2561	-0.0327	0.4090	0.2762	0.1216	1999 ± 167	2135 ± 280	2363 ± 166	3051 ± 151
202270_at	GBP1	guanylate binding protein 1, interferon-inducible	0.4795	-0.0005	0.4933	-0.0312	0.0459	84 ± 17	90 ± 16	154 ± 26	164 ± 33
202748_at	GBP2	guanylate binding protein 2, interferon-inducible	0.0695	-0.0181	0.4744	-0.3312	0.0968	261 ± 48	207 ± 28	288 ± 38	375 ± 48
218912_at	GCC1	golgi coiled coil 1	0.2364	-0.0155	-0.4072	0.3610	0.1502	397 ± 33	383 ± 12	466 ± 33	478 ± 44
202923_s_at	GCLC	glutamate-cysteine ligase, catalytic subunit	0.3378	-0.0329	-0.3315	-0.3267	0.3079	721 ± 30	772 ± 84	786 ± 79	890 ± 51
206397_x_at	GDF1	growth differentiation factor 1	0.0007	-0.0021	0.0047	0.1810	0.0013	3388 ± 448	3988 ± 621	4835 ± 615	9008 ± 1708
221314_at	GDF9	growth differentiation factor 9	0.2946	-0.0145	0.0757	-0.2874	0.0774	188 ± 17	194 ± 17	208 ± 19	285 ± 29
204472_at	GEM	GTP binding protein overexpressed in skeletal muscle	0.3951	-0.0200	-0.0220	-0.3777	0.1794	528 ± 93	462 ± 42	558 ± 82	775 ± 150
203540_at	GFAP	glial fibrillary acidic protein	0.0007	-0.0047	0.2849	-0.3598	0.0028	9575 ± 2303	2303 ± 2309	1655 ± 3370	1436 ± 3898
205100_at	GFPT2	glutamine-fructose-6-phosphate transaminase 2	0.0024	-0.0031	-0.1919	-0.2648	0.0390	473 ± 53	508 ± 63	534 ± 37	735 ± 100
208296_x_at	GG2-1	TNF-induced protein	0.0052	-0.0010	-0.1026	-0.3941	0.0051	137 ± 17	114 ± 10	176 ± 13	205 ± 24
50277_at	GGA1	golgi associated, γ adaptin ear containing, ARF BP 1	0.0087	-0.0094	0.1813	0.2164	0.0065	2115 ± 127	2236 ± 261	2197 ± 145	3273 ± 392
214233_at	GGA2	golgi associated, γ adaptin ear containing, ARF BP 2	0.2847	-0.0221	0.3788	-0.4479	0.0146	201 ± 28	234 ± 14	188 ± 23	336 ± 50
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	0.0578	-0.0398	0.1741	0.4364	0.2752	283 ± 21	262 ± 8	295 ± 27	330 ± 25
207131_x_at	GGT1	γ-glutamyltransferase 1	0.0498	-0.5682	0.3518	-0.3872	0.6655	228 ± 15	251 ± 32	242 ± 12	281 ± 57
218571_s_at	GIOT-3	GIOT-3 for gonadotropin inducible transcription repressor-3	0.0101	-0.0263	0.4362	0.4414	0.0373	385 ± 21	402 ± 20	479 ± 32	451 ± 22
201667_at	GJA1	gap junction protein, α 1, 43kDa	0.0088	-0.0029	0.2614	-0.0394	0.0066	8527 ± 616	9294 ± 933	1145 ± 1106	1958 ± 1320
204973_at	GJB1	gap junction protein, β 1, 32kDa	0.5627	-0.0024	-0.3942	-0.1613	0.0559	259 ± 33	245 ± 32	338 ± 31	414 ± 74
207034_s_at	GLI2	GLI-Kruppel family member GLI2	0.0394	-0.0313	0.0002	-0.0537	0.0126	53 ± 6	94 ± 16	93 ± 8	96 ± 1
208240_s_at	GLIO703	add fibroblast growth factor-like protein	0.0193	-0.4557	0.1676	-0.2935	0.4785	436 ± 71	591 ± 110	626 ± 85	608 ± 137
216021_s_at	GLRA3	glycine receptor, α 3	0.2047	-0.0032	-0.1144	-0.2517	0.0145	69 ± 19	53 ± 12	67 ± 12	134 ± 22
217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	0.0973	-0.0335	0.0961	0.3195	0.0610	5524 ± 762	5032 ± 1154	5937 ± 422	9236 ± 1566
222251_s_at	GMEB2	glucocorticoid modulatory element binding protein 2	0.0036	-0.0040	-0.0161	0.0936	0.0060	456 ± 17	447 ± 57	510 ± 45	748 ± 102
202543_s_at	GMFB	glia maturation factor, β	0.0300	-0.2118	0.4027	-0.4285	0.0298	258 ± 26	283 ± 36	436 ± 57	312 ± 50
218350_s_at	GMNN	geminin, DNA replication inhibitor	0.1277	-0.0363	-0.4888	-0.3441	0.2385	557 ± 48	531 ± 44	677 ± 69	691 ± 92
204187_at	GMPR	guanosine monophosphate reductase	0.0020	-0.0003	-0.2771	-0.0474	0.0068	302 ± 34	346 ± 63	558 ± 102	663 ± 97
214431_at	GMPS	guanine monophosphate synthetase	0.0463	-0.3648	0.1747	0.3103	0.5494	224 ± 24	224 ± 8	265 ± 28	265 ± 40
221737_at	GNA12	guanine nucleotide binding protein α 12	0.0009	-0.0057	0.1159	0.3704	0.0240	683 ± 54	714 ± 119	949 ± 83	1050 ± 119
201180_s_at	GNAI3	G Protein, α inhibiting activity polypeptide 3	0.1123	-0.0083	0.3466	-0.0228	0.0947	946 ± 113	1147 ± 112	1067 ± 82	1310 ± 81

Web Table 5 (13)

Probe set	Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
204993_at	GNAZ	guanine nucleotide binding protein, α z polypeptide	0.0099	-0.0145	0.0088	-0.0983	0.0075	943 \pm 54	1089 \pm 18	1052 \pm 71	1320 \pm 104
203363_s_at	GOLGA1	golgi autoantigen, golgin subfamily a, 1	0.2846	-0.0406	-0.0077	0.1321	0.0387	562 \pm 48	476 \pm 28	527 \pm 40	673 \pm 55
202106_at	GOLGA3	golgi autoantigen, golgin subfamily a, 3	0.0078	-0.1783	0.1386	-0.3005	0.4777	578 \pm 32	640 \pm 43	632 \pm 57	698 \pm 81
201567_s_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	0.5147	-0.0185	0.4713	-0.0085	0.2212	740 \pm 42	859 \pm 75	879 \pm 78	934 \pm 62
201056_at	GOLGB1	golgi autoantigen, golgin subfamily b, macrogolgin, 1	0.0162	-0.1767	0.4898	-0.4079	0.3962	591 \pm 38	653 \pm 70	653 \pm 42	736 \pm 79
204324_s_at	GOLPH4	golgi phosphoprotein 4	0.0002	-0.0585	0.0616	0.3239	0.1384	194 \pm 24	176 \pm 18	283 \pm 35	308 \pm 77
204630_s_at	GOSR1	golgi SNAP receptor complex member 1	0.0004	-0.0829	0.1248	-0.0587	0.2339	1205 \pm 69	1251 \pm 38	1597 \pm 206	1693 \pm 345
213205_at	GOSR2	golgi SNAP receptor complex member 2	0.0171	-0.2925	0.3581	-0.0243	0.1655	82 \pm 14	96 \pm 16	139 \pm 13	125 \pm 31
222058_at	GP	golliath protein	0.0234	-0.0021	-0.2028	-0.3028	0.0280	364 \pm 41	402 \pm 38	410 \pm 46	554 \pm 48
204984_at	GPC4	glypican 4	0.1666	-0.0028	0.3112	-0.2522	0.0219	252 \pm 27	306 \pm 38	333 \pm 41	413 \pm 33
209167_at	GPM6B	glycoprotein M6B	0.2911	-0.0011	0.4608	-0.1684	0.0396	5522 \pm 1053	15349 \pm 337	18872 \pm 810	9279 \pm 1359
214605_x_at	GPR1	G protein-coupled receptor 1	0.0121	-0.1013	-0.1805	0.1836	0.1079	99 \pm 16	66 \pm 18	111 \pm 18	166 \pm 50
211977_at	GPR107	G protein-coupled receptor 107	0.1652	-0.0414	0.0094	-0.4349	0.0648	280 \pm 16	355 \pm 44	305 \pm 22	423 \pm 61
220565_at	GPR2	G protein-coupled receptor 2	0.0626	-0.0228	-0.4947	0.1235	0.0097	137 \pm 13	123 \pm 21	135 \pm 15	229 \pm 36
206360_at	GPR23	G protein-coupled receptor 23	0.0237	-0.5581	0.0386	-0.0143	0.2369	61 \pm 9	86 \pm 17	97 \pm 12	76 \pm 12
206236_at	GPR4	G protein-coupled receptor 4	0.1179	-0.0222	0.1394	-0.3591	0.0902	131 \pm 15	166 \pm 34	164 \pm 19	221 \pm 29
206361_at	GPR44	G protein-coupled receptor 44	0.0698	-0.0232	0.2274	-0.0518	0.0404	158 \pm 15	193 \pm 28	161 \pm 19	261 \pm 44
213880_at	GPR49	G protein-coupled receptor 49	-0.9864	-0.0292	-0.4843	-0.3200	0.3585	310 \pm 22	269 \pm 26	391 \pm 74	392 \pm 71
212070_at	GPR56	G protein-coupled receptor 56	0.0227	-0.0076	0.0824	-0.2145	0.0914	2205 \pm 241	2498 \pm 267	2691 \pm 85	2995 \pm 154
206002_at	GPR64	G protein-coupled receptor 64	0.4096	-0.0444	-0.1669	-0.2039	0.1291	94 \pm 12	112 \pm 16	134 \pm 17	138 \pm 9
214467_at	GPR65	G protein-coupled receptor 65	0.0978	-0.0058	0.2720	-0.0545	0.0601	65 \pm 8	92 \pm 12	119 \pm 23	126 \pm 19
203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.5907	-0.0031	-0.1174	-0.2951	0.0812	9378 \pm 775	10323 \pm 997	10702 \pm 893	2968 \pm 1196
204396_s_at	GPRK5	G protein-coupled receptor kinase 5	0.0191	-0.0829	0.3653	-0.2351	0.1079	260 \pm 18	286 \pm 30	292 \pm 23	357 \pm 35
210981_s_at	GPRK6	G protein-coupled receptor kinase 6	0.0252	-0.3525	-0.4139	-0.3627	0.3867	253 \pm 32	306 \pm 45	340 \pm 45	327 \pm 36
214091_s_at	GPX3	glutathione peroxidase 3	0.0722	-0.0468	-0.4047	0.1236	0.1524	487 \pm 69	402 \pm 27	536 \pm 54	999 \pm 377
205068_s_at	GRAF	GTPase regulator associated with focal adhesion kinase pp125	0.0163	-0.0480	-0.2873	-0.4590	0.1240	363 \pm 18	347 \pm 20	358 \pm 35	448 \pm 44
210999_s_at	GRB10	growth factor receptor-bound protein 10	0.0198	-0.0152	-0.0308	0.3708	0.0133	195 \pm 25	149 \pm 18	204 \pm 20	329 \pm 62
212244_at	GRINL1A	glutamate receptor, ionotropic, NMDA-like 1A	0.1951	-0.0272	-0.2613	-0.1004	0.3773	735 \pm 71	761 \pm 78	834 \pm 76	901 \pm 26
208035_at	GRM6	glutamate receptor, metabotropic 6	0.1456	-0.0001	0.2317	-0.0015	0.0001	281 \pm 17	306 \pm 24	286 \pm 29	492 \pm 46
205801_s_at	GRP3	guanine nucleotide exchange factor for Rap1	0.1053	-0.0016	0.3245	0.4359	0.0067	263 \pm 33	223 \pm 36	493 \pm 94	494 \pm 64
209945_s_at	GSK3B	glycogen synthase kinase 3 β	0.0279	-0.0703	0.1926	-0.0481	0.0448	419 \pm 24	548 \pm 55	559 \pm 18	616 \pm 77
210912_x_at	GSTM4	glutathione S-transferase M4	0.1168	-0.0165	0.4771	-0.0925	0.0192	474 \pm 30	511 \pm 45	462 \pm 17	591 \pm 12
205752_s_at	GSTM5	glutathione S-transferase M5	0.0035	-0.0005	0.4310	-0.4405	0.0088	1039 \pm 164	997 \pm 93	1324 \pm 157	1926 \pm 287
205439_at	GSTT2	glutathione S-transferase theta 2	0.0609	-0.0499	-0.2853	-0.3129	0.1187	107 \pm 16	147 \pm 30	133 \pm 29	195 \pm 23
222451_at	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	0.0620	-0.0467	0.0252	-0.1414	0.0349	653 \pm 49	743 \pm 56	894 \pm 63	815 \pm 59
222104_x_at	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	0.0188	-0.0183	0.0120	-0.1941	0.0192	267 \pm 26	447 \pm 70	546 \pm 75	523 \pm 79
210891_s_at	GTF2I	general transcription factor II, i	0.2744	-0.0106	0.4968	-0.0119	0.0945	7358 \pm 359	7783 \pm 546	8911 \pm 158	8478 \pm 660
35871_at	GTF3C1	general transcription factor IIIC, polypeptide 1, α	0.0886	-0.2387	-0.2871	0.1669	0.2613	1670 \pm 76	1675 \pm 150	2015 \pm 130	2016 \pm 274
204366_s_at	GTF3C2	general transcription factor IIIC, polypeptide 2, β	0.2079	-0.0237	-0.2871	-0.2680	0.0363	902 \pm 49	983 \pm 106	856 \pm 43	1247 \pm 162
213835_x_at	GTPBG3	mitochondrial GTP binding protein	0.0418	-0.1445	0.0926	-0.2526	0.3571	493 \pm 36	569 \pm 63	572 \pm 50	634 \pm 76
218088_s_at	GTR2	Rag C protein	0.0001	-0.0002	-0.4090	0.2745	0.0007	1041 \pm 36	1013 \pm 82	1218 \pm 67	1411 \pm 69
211040_x_at	GTSE1	G-2 and S-phase expressed 1	0.3915	-0.0119	-0.1952	-0.1168	0.2177	848 \pm 64	867 \pm 25	926 \pm 51	1045 \pm 102

Web Table 5 (14)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
202605_at	GUSB	glucuronidase, β	0.0180	-0.2020	-0.3251	0.4929	0.4342	628 \pm 68	704 \pm 87	685 \pm 28	873 \pm 195
215695_s_at	GYG2	glycogenin 2	0.0496	-0.0128	0.1616	-0.0860	0.1524	155 \pm 25	150 \pm 29	198 \pm 25	227 \pm 24
216833_x_at	GYPB	glycophorin B	0.3405	-0.0236	0.0623	-0.1498	0.1241	133 \pm 20	124 \pm 17	165 \pm 14	190 \pm 27
215093_at	H105E3	NAD dependent steroid dehydrogenase-like; H105e3	0.0019	-0.0135	0.2719	-0.0205	0.0545	187 \pm 12	219 \pm 14	229 \pm 11	258 \pm 28
221667_s_at	H11	protein kinase H11	0.0325	-0.0110	-0.2135	-0.1292	0.2250	3080 \pm 407	3136 \pm 396	3949 \pm 579	4552 \pm 813
208398_at	H1F2	H1 histone family, member 2	0.0026	0.0000	-0.4224	-0.1851	0.0012	200 \pm 21	197 \pm 19	292 \pm 20	424 \pm 74
204805_s_at	H1FX	H1 histone family, member X	0.3343	-0.0103	0.2358	0.1958	0.0086	802 \pm 157	717 \pm 47	750 \pm 37	1503 \pm 271
220936_s_at	H2AFJ	H2A histone family, member J	0.0934	-0.0112	0.4641	-0.0283	0.0453	95 \pm 12	100 \pm 17	91 \pm 12	145 \pm 16
218280_x_at	H2AFO	H2A histone family, member O	0.0516	-0.0376	-0.0310	0.1351	0.0355	336 \pm 21	281 \pm 25	254 \pm 30	443 \pm 86
205436_s_at	H2AFX	H2A histone family, member X	0.1529	-0.0294	0.2264	0.1686	0.0226	1393 \pm 98	1471 \pm 142	1372 \pm 81	1995 \pm 252
212205_at	H2AV	histone H2A.F/Z variant	0.0383	-0.1289	0.1438	-0.0485	0.0417	3246 \pm 90	3551 \pm 178	4050 \pm 157	3704 \pm 314
222067_x_at	H2BFB	H2B histone family, member B	0.1840	-0.0138	-0.0056	0.0508	0.0319	232 \pm 18	192 \pm 18	197 \pm 35	359 \pm 71
202708_s_at	H2BFQ	H2B histone family, member Q	0.2363	-0.0142	-0.1293	0.0513	0.0888	898 \pm 127	681 \pm 39	867 \pm 86	1271 \pm 256
211940_x_at	H3F3A	H3 histone, family 3A	0.9045	-0.0299	-0.1043	0.3697	0.0458	5312 \pm 467	4361 \pm 327	4678 \pm 194	6807 \pm 1017
211938_at	H3F3B	H3 histone, family 3B	0.0179	-0.0191	0.0119	-0.3470	0.0432	1123 \pm 66	1487 \pm 171	1755 \pm 138	1810 \pm 328
208181_at	H4FH	H4 histone family, member H	0.0170	-0.0073	0.3022	0.1819	0.0110	35 \pm 7	28 \pm 6	39 \pm 11	80 \pm 16
208630_at	HADHA	enoyl-Coenzyme A hydratase, α subunit	0.0118	-0.0521	0.4725	0.2224	0.0996	688 \pm 47	605 \pm 39	803 \pm 76	853 \pm 99
221745_at	HAN11	WD-repeat protein	0.3014	-0.0207	0.2287	-0.1814	0.2937	353 \pm 43	329 \pm 12	415 \pm 27	451 \pm 79
220801_s_at	HAO2	hydroxyacid oxidase 2	0.1094	-0.0016	0.0467	-0.0357	0.0027	145 \pm 12	200 \pm 20	176 \pm 20	288 \pm 42
209102_s_at	HBP1	HMG-box containing protein 1	0.0481	-0.0149	-0.0662	-0.2922	0.1785	862 \pm 68	836 \pm 71	1029 \pm 104	1062 \pm 94
218166_s_at	HBXAP	hepatitis B virus x associated protein	0.0084	-0.0001	-0.3952	-0.0954	0.0067	182 \pm 15	170 \pm 17	219 \pm 12	251 \pm 19
218682_s_at	HCAP-G	chromosome condensation protein G	0.2099	-0.0134	0.0298	-0.2702	0.0556	53 \pm 6	80 \pm 13	68 \pm 17	107 \pm 17
216229_x_at	HCGII-7	HCGII-7 protein	0.0073	-0.0217	0.0403	-0.4671	0.0494	468 \pm 49	475 \pm 56	589 \pm 57	672 \pm 92
217965_s_at	HCNGP	transcriptional regulator protein	0.1128	-0.0199	0.2201	-0.1481	0.1208	306 \pm 15	374 \pm 52	394 \pm 48	526 \pm 88
42361_g_at	HCR	HCR	0.0006	-0.1657	0.2218	-0.4724	0.3324	98 \pm 9	113 \pm 15	117 \pm 16	143 \pm 26
201209_at	HDAC1	histone deacetylase 1	0.0383	-0.0168	0.2007	-0.1396	0.0366	487 \pm 57	591 \pm 78	749 \pm 66	680 \pm 61
204225_at	HDAC4	histone deacetylase 4	0.1689	-0.0037	-0.2877	0.2746	0.0177	444 \pm 34	410 \pm 20	484 \pm 34	579 \pm 42
217937_s_at	HDAC7A	histone deacetylase 7A	0.0145	-0.1376	0.1337	-0.3190	0.0779	169 \pm 29	200 \pm 42	306 \pm 21	258 \pm 56
212765_s_at	HDCMA18P	HDCMA18P protein	0.6277	-0.0403	0.3208	-0.0189	0.2753	437 \pm 37	520 \pm 45	520 \pm 41	530 \pm 30
200896_x_at	HDGF	hepatoma-derived growth factor	0.1432	-0.0302	-0.0260	-0.4717	0.2466	1827 \pm 135	1806 \pm 54	1899 \pm 78	2144 \pm 185
203674_at	HELZ	helicase with zinc finger domain	0.0327	-0.9466	0.4966	0.4583	0.4163	984 \pm 56	1153 \pm 118	1168 \pm 53	1079 \pm 124
203903_s_at	HEPH	hephaestin	0.0097	-0.0143	0.4726	-0.3213	0.0041	809 \pm 59	802 \pm 57	1139 \pm 33	1007 \pm 107
206087_x_at	HFE	hemochromatosis	0.0204	-0.1680	0.0694	0.1289	0.1289	303 \pm 22	380 \pm 57	419 \pm 14	415 \pm 47
206910_x_at	HFL3	H factor-like 3	0.1493	-0.0194	0.0671	-0.2142	0.0244	164 \pm 20	200 \pm 7	179 \pm 15	242 \pm 19
217130_at	HFSE-1	HFSE-1 protein	0.0252	-0.2062	0.4533	0.4596	0.3994	251 \pm 24	263 \pm 40	281 \pm 32	334 \pm 48
209960_at	HGF	hepatocyte growth factor	0.0058	-0.0061	0.3819	-0.1260	0.0037	61 \pm 8	56 \pm 12	106 \pm 12	95 \pm 9
209558_s_at	HIP12	huntingtin interacting protein 12	0.0017	-0.0211	0.1561	0.4829	0.0613	1415 \pm 66	1747 \pm 160	2174 \pm 93	2530 \pm 580
219028_at	HIPK2	homeodomain interacting protein kinase 2	0.0100	-0.0715	0.1187	-0.2245	0.1298	801 \pm 125	1247 \pm 214	1548 \pm 266	1356 \pm 327
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP α 1	0.1330	-0.0039	0.0403	-0.0453	0.0316	115 \pm 19	177 \pm 30	218 \pm 39	245 \pm 31
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR β 4	0.5562	-0.0241	-0.4147	-0.2074	0.1962	64 \pm 31	255 \pm 93	328 \pm 126	365 \pm 143
209094_at	HLA-E	major histocompatibility complex, class I, E	0.0412	-0.0143	0.2928	-0.4695	0.0838	802 \pm 84	838 \pm 102	1191 \pm 194	1169 \pm 129
207565_s_at	HLALS	major histocompatibility complex, class II-like sequence	0.0540	-0.0034	0.1439	-0.0397	0.0099	56 \pm 8	64 \pm 11	59 \pm 12	112 \pm 16

Web Table 5 (15)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
209399_at	HLCS	0.3150	-0.0340	0.1826	-0.1758	0.1571	298 ± 20	296 ± 10	299 ± 22	369 ± 40
203040_s_at	HMBS	0.6340	-0.0112	-0.0865	-0.4070	0.0658	380 ± 30	387 ± 36	363 ± 17	495 ± 56
219959_at	HMCS	0.9247	-0.0283	0.2754	0.3527	0.1241	88 ± 14	76 ± 10	75 ± 8	134 ± 31
210719_s_at	HMGB2B	0.0729	-0.0051	0.1253	-0.2553	0.0067	267 ± 27	385 ± 36	344 ± 25	458 ± 50
203744_at	HMGB3	0.1438	-0.0269	0.0253	-0.0227	0.1632	568 ± 20	585 ± 30	642 ± 25	697 ± 79
202772_at	HMGBL	0.0799	-0.0355	0.1149	0.2023	0.1349	617 ± 24	841 ± 70	704 ± 38	783 ± 83
209377_s_at	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	0.5215	-0.0142	-0.0168	-0.1120	0.0340	3728 ± 155	3686 ± 480	4919 ± 422	4500 ± 209
203665_at	high mobility group nucleosomal binding domain 3	0.3369	-0.0480	-0.0964	0.4185	0.2454	542 ± 62	446 ± 13	518 ± 42	649 ± 100
203665_at	heme oxygenase 1	0.0011	-0.0131	-0.2089	0.1081	0.0259	211 ± 19	181 ± 17	268 ± 25	343 ± 68
212109_at	HN1 like	0.0088	-0.0475	-0.0056	-0.4787	0.1727	1718 ± 140	1554 ± 46	1834 ± 106	2140 ± 225
214280_x_at	heterogeneous nuclear ribonucleoprotein A1	0.0363	-0.0458	-0.1545	-0.1360	0.3048	383 ± 26	419 ± 49	417 ± 45	508 ± 69
210110_x_at	heterogeneous nuclear ribonucleoprotein H3	0.0839	-0.0330	0.2808	-0.0780	0.1649	874 ± 44	951 ± 123	975 ± 81	1197 ± 142
200072_s_at	heterogeneous nuclear ribonucleoprotein M	0.0285	-0.0003	0.2780	-0.3614	0.0011	438 ± 54	492 ± 81	614 ± 32	879 ± 109
204647_at	Homer, neuronal immediate early gene, 3	0.1568	-0.0235	0.1134	-0.0650	0.1396	235 ± 25	287 ± 30	329 ± 34	383 ± 81
206848_at	homeo box A7	0.0237	-0.0572	0.0509	-0.0233	0.0765	277 ± 24	379 ± 36	342 ± 31	461 ± 85
205600_x_at	homeo box B5	0.0040	-0.0004	0.0495	-0.0181	0.0030	153 ± 14	189 ± 20	167 ± 18	295 ± 46
206194_at	homeo box C4	0.0008	-0.0133	0.0638	-0.3815	0.0099	1382 ± 115	1987 ± 266	2668 ± 314	2541 ± 222
214177_s_at	hematopoietic PBX-interacting protein	0.4048	-0.0029	0.4627	0.2943	0.0029	65 ± 4	63 ± 11	62 ± 7	126 ± 23
221170_at	histamine H4 receptor	0.0042	-0.0021	0.0635	-0.0825	0.0193	711 ± 69	768 ± 84	951 ± 117	1468 ± 321
216210_x_at	Tara-like protein	0.0087	-0.2161	-0.4997	-0.2943	0.6701	1239 ± 83	1279 ± 108	1313 ± 85	1404 ± 116
202099_s_at	HMT1 hnRNP methyltransferase-like 1	0.8275	-0.0298	0.0850	-0.0597	0.1046	226 ± 18	275 ± 18	310 ± 16	336 ± 58
203395_s_at	hair cell homolog	0.1550	-0.0449	0.0280	-0.0483	0.1457	182 ± 14	200 ± 27	245 ± 19	236 ± 25
203283_s_at	heparan sulfate 2-O-sulfotransferase 1	0.3976	-0.0047	0.3018	-0.0278	0.0323	1139 ± 32	1173 ± 42	1158 ± 25	1387 ± 119
217760_at	DIPB protein	0.0008	-0.1117	0.2660	0.4488	0.1461	562 ± 27	599 ± 47	595 ± 47	708 ± 59
200941_at	transcription factor	0.0483	-0.1191	0.3705	-0.1979	0.5439	1858 ± 112	1786 ± 145	2012 ± 130	2056 ± 199
220081_x_at	heat shock factor binding protein 1	0.0012	-0.0018	0.0627	-0.1158	0.0182	664 ± 70	935 ± 112	1138 ± 128	1248 ± 190
221771_s_at	hydroxysteroid dehydrogenase 7	0.0335	-0.0193	-0.3458	-0.3883	0.1061	1038 ± 58	985 ± 28	1152 ± 62	1215 ± 104
218826_at	M-phase phosphoprotein, mpp8	0.0117	-0.0068	0.0375	-0.0022	0.0004	349 ± 28	544 ± 56	451 ± 31	590 ± 35
205824_at	novel protein	0.0792	-0.0101	-0.4014	-0.2725	0.0544	241 ± 36	244 ± 32	374 ± 37	373 ± 70
219284_at	HSPB associated protein 1	0.0321	-0.0871	-0.1388	-0.3041	0.3554	306 ± 40	322 ± 12	332 ± 24	385 ± 38
219357_at	HSPB1	0.0042	-0.0086	0.1314	-0.4463	0.0256	567 ± 26	545 ± 35	813 ± 65	901 ± 168
218936_s_at	HSPC018 protein	0.0594	-0.0119	0.3851	-0.0222	0.1222	325 ± 11	348 ± 31	354 ± 28	434 ± 54
221046_s_at	HSPC128 protein	0.0003	-0.0720	0.3881	-0.4735	0.1749	535 ± 42	527 ± 53	601 ± 51	762 ± 148
214328_s_at	HSPC135 protein	0.1638	-0.0187	-0.0232	0.3004	0.0833	1402 ± 1190	3042 ± 1353	1437 ± 1827	5463 ± 2900
213545_at	heat shock 90kDa protein 1, α	0.0150	-0.0187	-0.0232	0.3004	0.0833	368 ± 48	511 ± 95	669 ± 156	688 ± 233
209360_s_at	rTS β protein	0.4625	-0.2776	0.0081	0.3794	0.3304	264 ± 28	302 ± 30	293 ± 30	372 ± 65
209448_at	endogenous retrovirus HD1/ ORF1/ ORF2/ envelope protein	0.0003	-0.0052	-0.4350	-0.1846	0.0702	437 ± 40	489 ± 67	630 ± 66	684 ± 104
206639_x_at	HIV-1 Tat interactive protein 2, 30kDa	0.2992	-0.0285	0.1227	-0.1586	0.0100	72 ± 13	103 ± 21	60 ± 11	158 ± 33
205956_x_at	histatin 1	0.0035	-0.0235	0.0304	-0.4651	0.0162	232 ± 15	335 ± 62	326 ± 26	402 ± 33
213230_at	GT198, complete ORF	0.0069	-0.0184	-0.2988	0.3277	0.1046	308 ± 35	343 ± 57	412 ± 31	534 ± 121
201906_s_at	paraneoplastic antigen	0.0099	-0.0080	-0.4795	-0.3534	0.0472	565 ± 54	607 ± 47	738 ± 41	738 ± 65
212493_s_at	HYA22 protein	0.0589	-0.0002	-0.2118	-0.3614	0.0062	760 ± 40	677 ± 35	959 ± 66	1050 ± 123
	Huntingtin interacting protein B									

Web Table 5 (16)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
219910_at	HYPE	Huntingtin interacting protein E	0.0167	-0.0208	0.3751	0.3312	0.0189	385 ± 33	421 ± 49	437 ± 35	622 ± 89
64064_at	IAN4L1	Immune associated nucleotide 4 like 1	0.3988	-0.0081	0.2504	-0.0512	0.0912	798 ± 100	892 ± 58	862 ± 52	1135 ± 137
202638_s_at	ICAM-1	Intercellular adhesion molecule 1, human rhinovirus receptor	0.7981	-0.0215	0.2416	-0.1320	0.1649	145 ± 22	178 ± 22	176 ± 4	212 ± 25
203337_x_at	ICAM-1A	Integrin cytoplasmic domain-associated protein 1	0.1185	-0.0163	0.3539	-0.3135	0.0183	639 ± 91	486 ± 91	568 ± 42	856 ± 65
207826_s_at	ID3	Inhibitor of DNA binding 3, dominant (-) HLH protein	0.5310	-0.0253	-0.0239	-0.4252	0.0887	330 ± 61	265 ± 75	505 ± 35	424 ± 83
209292_at	ID4	Inhibitor of DNA binding 4, dominant (-) HLH protein	0.4504	-0.0427	0.1727	-0.0110	0.2324	918 ± 142	1154 ± 160	1429 ± 245	1321 ± 192
210045_at	IDH2	isocitrate dehydrogenase 2, mitochondrial	0.0491	-0.1209	0.1369	-0.0940	0.3844	634 ± 59	811 ± 126	869 ± 78	960 ± 244
212483_at	IDN3	IDN3 protein	0.0020	-0.0039	0.2102	-0.3477	0.0188	425 ± 37	454 ± 44	570 ± 24	604 ± 68
205068_at	IDUA	Iduronidase, α-L-	0.0112	-0.0736	0.1242	-0.0002	0.4207	136 ± 17	176 ± 24	178 ± 20	200 ± 38
214314_s_at	IF2	translation initiation factor IF2	0.0593	-0.0046	0.0239	-0.1421	0.0879	149 ± 21	176 ± 29	212 ± 36	264 ± 38
208965_s_at	IF16	interferon, γ-inducible protein 16	0.0073	-0.0071	0.4553	-0.0544	0.0483	124 ± 22	139 ± 19	162 ± 4	203 ± 24
201315_x_at	IFITM2	interferon induced transmembrane protein 2	0.3289	-0.0388	-0.0310	-0.4588	0.3639	2361 ± 394	2300 ± 275	2505 ± 283	3232 ± 571
208448_x_at	IFNA16	interferon, α 16	0.4667	-0.0035	0.1753	0.4397	0.0072	128 ± 11	106 ± 11	122 ± 8	180 ± 22
214569_at	IFNA5	interferon, α 5	0.2400	-0.0137	0.0216	-0.0291	0.0697	101 ± 10	117 ± 15	118 ± 13	175 ± 34
210354_at	IFNG	interferon, γ	0.5036	-0.0139	0.0368	-0.0010	0.0536	110 ± 11	154 ± 22	119 ± 16	189 ± 32
209100_at	IFRD2	interferon-related developmental regulator 2	0.0966	-0.0379	-0.3982	0.2574	0.2415	559 ± 51	610 ± 62	699 ± 60	722 ± 85
203628_at	IGF1R	insulin-like growth factor 1 receptor	0.2267	-0.0416	0.1521	-0.0860	0.0931	244 ± 40	320 ± 39	483 ± 104	414 ± 51
203425_s_at	IGFBP5	insulin-like growth factor binding protein 5	0.0141	-0.1448	0.3618	0.0852	0.2220	144 ± 12	130 ± 15	158 ± 14	182 ± 24
221453_at	IGRP	islet-specific G6P catalytic subunit-related protein	0.0275	-0.0103	0.2944	-0.3287	0.0052	285 ± 28	336 ± 42	311 ± 14	509 ± 76
206420_at	IGSF6	immunoglobulin superfamily, member 6	0.1250	-0.0056	0.1719	-0.2739	0.0135	77 ± 9	91 ± 8	87 ± 13	129 ± 13
204912_at	IL10RA	interleukin 10 receptor, α	0.0029	0.0000	0.0744	-0.0319	0.0006	247 ± 18	309 ± 23	333 ± 32	473 ± 57
209575_at	IL10RB	interleukin 10 receptor, β	0.0476	-0.0406	0.0583	-0.0116	0.1471	180 ± 17	244 ± 21	233 ± 28	269 ± 43
201887_at	IL13RA1	interleukin 13 receptor, α 1	0.2656	-0.0087	0.0103	-0.0713	0.0294	618 ± 64	815 ± 64	768 ± 66	918 ± 79
212300_at	IL14	Interleukin 14	0.0148	-0.0722	-0.2701	-0.2278	0.0018	404 ± 25	375 ± 39	576 ± 35	455 ± 40
217371_s_at	IL15	Interleukin 15	0.4004	-0.0023	0.1822	-0.1245	0.0124	47 ± 7	50 ± 7	55 ± 8	86 ± 10
205707_at	IL17R	interleukin 17 receptor	0.4245	-0.0297	0.0266	-0.2735	0.1405	427 ± 39	498 ± 53	540 ± 72	641 ± 77
206295_at	IL18	interleukin 18	0.2454	-0.0423	0.1406	-0.0014	0.3269	70 ± 13	88 ± 13	84 ± 10	109 ± 22
208200_at	IL1A	interleukin 1, α	0.0236	-0.0002	0.2490	-0.4684	0.0029	98 ± 9	102 ± 14	112 ± 10	159 ± 6
202948_at	IL1R1	interleukin 1 receptor, type I	0.0593	-0.0185	0.3273	-0.1392	0.0525	353 ± 63	461 ± 89	605 ± 61	547 ± 51
220563_at	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	0.1197	-0.0447	-0.3947	-0.4324	0.1236	824 ± 66	895 ± 89	1134 ± 124	1028 ± 110
220056_at	IL22R	interleukin 22 receptor	0.0121	-0.0863	0.4088	0.4312	0.1247	167 ± 12	182 ± 29	189 ± 18	247 ± 36
204116_at	IL2RG	interleukin 2 receptor, γ	-0.8498	-0.0379	0.0390	-0.0105	0.4319	338 ± 34	394 ± 33	428 ± 30	421 ± 60
205207_at	IL6	Interleukin 6	-0.8048	-0.0436	-0.3757	-0.3026	0.0573	148 ± 14	163 ± 23	130 ± 21	227 ± 37
205945_at	IL6R	interleukin 6 receptor	0.3942	-0.0098	0.0431	-0.1237	0.0575	138 ± 14	157 ± 17	178 ± 15	204 ± 20
204863_s_at	IL6ST	interleukin 6 signal transducer	0.0045	-0.0988	0.2054	-0.0903	0.1647	240 ± 21	259 ± 23	326 ± 17	313 ± 56
221548_s_at	ILKAP	integrin-linked kinase-assoc. serine/threonine ptase 2C	0.0050	-0.0188	0.3352	0.3466	0.0346	386 ± 23	402 ± 26	450 ± 33	552 ± 71
215838_at	ILT11	leukocyte immunoglobulin-like receptor, B 7	0.0840	-0.0273	0.2746	-0.2116	0.1102	75 ± 15	95 ± 20	104 ± 7	131 ± 18
205581_s_at	ING1L	inhibitor of growth family, member 1-like	0.4275	-0.0276	-0.2699	0.1529	0.0500	276 ± 28	270 ± 30	269 ± 31	376 ± 27
205070_at	ING3	inhibitor of growth family, member 3	0.0279	-0.0308	-0.2624	-0.4706	0.0134	353 ± 37	317 ± 23	485 ± 49	420 ± 11
48825_at	ING4	candidate tumor suppressor p33 ING1 homolog	0.1851	-0.0393	-0.0523	-0.1946	0.2793	393 ± 16	383 ± 39	453 ± 34	447 ± 32
202794_at	INPP1	inositol polyphosphate-1-phosphatase	0.4936	-0.0044	-0.4137	-0.4802	0.0315	1793 ± 74	1683 ± 164	1780 ± 80	2192 ± 137
201598_s_at	INPPL1	inositol polyphosphate phosphatase-like 1	0.0032	-0.0573	0.1656	-0.4308	0.0901	438 ± 36	578 ± 61	547 ± 44	658 ± 97

Web Table 5 (17)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
201625_s_at	INSIG1	insulin induced gene 1	0.2819	-0.0216	-0.2624	0.2973	0.1513	207 ± 23	197 ± 30	229 ± 35	291 ± 30
213792_s_at	INSR	insulin receptor	0.0001	-0.0122	0.3332	0.2521	0.0168	630 ± 54	702 ± 88	846 ± 106	1319 ± 279
219843_at	IPP	intracisternal A particle-promoted polypeptide	0.0356	-0.0841	0.0191	-0.0551	0.1628	153 ± 22	226 ± 37	193 ± 14	241 ± 43
221974_at	IPW	imprinted in Prader-Willi syndrome	0.0170	-0.0071	-0.3939	-0.0576	0.0763	391 ± 46	393 ± 53	545 ± 80	550 ± 30
213446_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	0.0390	-0.1261	-0.0497	0.3772	0.0998	113 ± 19	110 ± 5	121 ± 11	174 ± 32
203474_at	IQGAP2	IQ motif containing GTPase activating protein 2	0.0022	-0.0607	-0.0679	0.3583	0.0697	80 ± 13	83 ± 13	91 ± 10	150 ± 36
201587_s_at	IRAK1	interleukin-1 receptor-associated kinase 1	0.2154	-0.0004	0.1876	-0.3026	0.0109	828 ± 81	819 ± 87	1121 ± 103	1294 ± 157
219618_at	IRAK4	interleukin-1 receptor-associated kinase 4	0.1283	-0.0010	0.2831	-0.1557	0.0120	85 ± 14	120 ± 12	128 ± 15	164 ± 21
202621_at	IRF3	interferon regulatory factor 3	0.0036	-0.0363	-0.0294	-0.4987	0.1216	421 ± 52	372 ± 50	480 ± 50	570 ± 72
208436_s_at	IRF7	interferon regulatory factor 7	0.1181	-0.0034	0.4770	-0.1925	0.0739	223 ± 37	223 ± 29	267 ± 31	425 ± 108
209184_s_at	IRS2	insulin receptor substrate 2	0.0469	-0.0162	0.2325	0.2139	0.0642	2760 ± 155	2867 ± 224	3221 ± 424	3863 ± 283
222126_at	IRS3L	insulin receptor substrate 3-like	0.0826	-0.0055	0.0235	-0.0016	0.0082	404 ± 19	573 ± 55	596 ± 59	611 ± 31
207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	0.0425	-0.2678	0.0411	-0.0151	0.3381	136 ± 15	197 ± 20	193 ± 37	212 ± 51
214660_at	ITGA1	integrin, α1	0.0126	-0.0056	0.1753	-0.0072	0.0405	17 ± 2	23 ± 5	22 ± 5	49 ± 15
206766_at	ITGA10	integrin, α10	0.1222	-0.0207	0.2957	-0.1090	0.0823	363 ± 35	379 ± 30	365 ± 13	470 ± 45
201656_at	ITGA6	integrin, α6	0.3613	-0.0391	0.0840	-0.0130	0.3150	369 ± 34	501 ± 75	508 ± 78	516 ± 77
216331_at	ITGA7	integrin, α7	0.0848	-0.0186	0.0047	0.4410	0.0169	794 ± 44	1013 ± 116	1377 ± 137	1358 ± 228
204990_s_at	ITGB4	integrin, β4	0.0000	-0.0027	0.2021	0.4038	0.0090	581 ± 102	733 ± 162	1106 ± 146	1302 ± 210
214020_x_at	ITGB5	integrin, β5	0.1007	-0.0029	0.4578	-0.0295	0.0715	301 ± 24	350 ± 54	414 ± 36	477 ± 75
205816_at	ITGB8	integrin, β8	0.0013	-0.0003	0.1977	-0.4076	0.0049	93 ± 14	104 ± 19	145 ± 16	171 ± 14
37201_at	ITIH4	inter-α-inhibitor H4	0.0124	-0.0286	0.1498	0.2076	0.3251	300 ± 21	342 ± 43	322 ± 26	429 ± 94
210740_s_at	ITPK1	inositol 1,3,4-trisphosphate 5/6 kinase	0.2014	-0.0094	0.4446	0.3792	0.0311	2826 ± 150	2665 ± 127	3357 ± 193	3334 ± 241
203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	0.0093	-0.0017	-0.1140	-0.3123	0.0230	2349 ± 446	2585 ± 171	4220 ± 708	4519 ± 781
213076_at	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	0.1334	-0.0097	-0.1257	-0.4305	0.0626	532 ± 35	531 ± 24	586 ± 42	761 ± 116
35776_at	ITSN1	intersectin 1	0.0484	-0.0081	0.4158	-0.3448	0.0504	894 ± 95	1048 ± 115	1069 ± 100	1367 ± 152
218517_at	Jade-1	PHD protein Jade-1	0.0016	-0.0002	-0.4109	0.3962	0.0008	529 ± 38	567 ± 53	658 ± 38	848 ± 75
207187_at	JAK3	Janus Kinase 3	0.1097	-0.0064	0.1080	-0.0339	0.1091	400 ± 21	444 ± 30	438 ± 35	540 ± 66
214037_s_at	JM1	JM1 protein	0.0116	-0.0699	0.2736	-0.4667	0.3091	95 ± 14	107 ± 12	105 ± 7	137 ± 26
209217_s_at	JM5	JM5 protein	0.0080	-0.0142	0.2165	-0.2095	0.0621	669 ± 31	678 ± 32	715 ± 52	841 ± 63
37872_at	JRK	jerky homolog	0.0757	-0.0002	0.0915	-0.0121	0.0076	283 ± 17	303 ± 17	339 ± 16	383 ± 26
213281_at	JUN	v-Jun sarcoma virus 17 oncogene homolog	0.0123	-0.0462	0.4313	0.4139	0.0326	231 ± 28	306 ± 39	288 ± 26	365 ± 21
203752_s_at	JUND	jun D proto-oncogene	0.0006	-0.0284	0.4697	-0.0494	0.1244	7987 ± 603	8307 ± 654	9983 ± 683	0792 ± 1603
222105_s_at	KBRAS2	kappa-B-interacting Ras-like protein 2	0.0013	-0.1363	0.0507	-0.2443	0.3500	221 ± 40	281 ± 34	343 ± 37	397 ± 142
205616_at	KCNA6	K+ channel, shaker-related subfamily, member 6	0.6276	-0.0233	-0.0192	0.3894	0.0328	201 ± 22	125 ± 25	237 ± 15	280 ± 63
220776_at	KCNJ14	K+ inwardly-rectifying channel, subfamily J, member 14	0.0166	-0.0011	0.0401	-0.0048	0.0048	110 ± 6	136 ± 12	132 ± 12	239 ± 47
211806_s_at	KCNJ15	K+ inwardly-rectifying channel, subfamily J, member 15	0.0213	-0.0012	0.0722	-0.0810	0.0117	275 ± 21	303 ± 23	339 ± 33	443 ± 50
220727_at	KCNK10	potassium channel, subfamily K, member 10	0.0043	-0.0101	0.0012	-0.1831	0.0120	126 ± 9	154 ± 21	153 ± 8	222 ± 33
219615_s_at	KCNK5	potassium channel, subfamily K, member 5	0.0036	-0.0001	-0.2003	0.2202	0.0001	116 ± 12	100 ± 16	141 ± 13	239 ± 31
219287_at	KCNMB4	K+ large conductance Ca++-activated channel, M, β4	0.0110	-0.0714	0.4940	0.2051	0.1329	1214 ± 88	1213 ± 124	1246 ± 76	1612 ± 217
205902_at	KCNN3	intermediate/small Ca++-activated K+ channel N3	0.0037	-0.0049	0.4348	-0.1493	0.0194	731 ± 117	798 ± 124	1374 ± 227	1393 ± 242
214185_at	KHDRBS1	KH dom. containing, RNA binding, signal transd. assoc. 1	0.1717	-0.0007	-0.1785	0.1870	0.0030	200 ± 17	168 ± 23	209 ± 20	306 ± 34
212303_x_at	KHSRP	KH-type splicing regulatory protein	0.0154	-0.8695	0.1610	-0.4943	0.4099	667 ± 42	794 ± 47	825 ± 87	748 ± 102

Web Table 5 (18)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
200906_s_at	KIAA0992	palladin	0.0060	-0.0407	-0.0466	0.4818	0.1323	140 ± 15	99 ± 17	164 ± 21	170 ± 33
222310_at	KIAA1172	pro-mRNA splicing SR protein rA4	0.0043	-0.0362	-0.3607	-0.2180	0.0429	220 ± 27	241 ± 33	360 ± 47	308 ± 40
202962_at	KIF13B	kinesin family member 13B	0.2037	-0.0255	0.3258	0.4888	0.0631	731 ± 60	895 ± 138	881 ± 81	1127 ± 140
206364_at	KIF14	kinesin family member 14	0.0313	-0.0046	0.1049	-0.1069	0.0348	45 ± 8	40 ± 8	61 ± 11	86 ± 15
203943_at	KIF3B	kinesin family member 3B	0.0037	-0.0697	0.0972	-0.2634	0.2003	1251 ± 98	1250 ± 61	1469 ± 117	1553 ± 178
201991_s_at	KIF5B	kinesin family member 5B	0.0339	-0.1585	-0.2502	-0.2047	0.5321	3698 ± 153	3734 ± 552	4224 ± 421	4506 ± 495
207029_at	KITLG	KIT ligand	0.0439	-0.0404	-0.3623	-0.1597	0.0622	65 ± 8	55 ± 6	80 ± 4	76 ± 6
210504_at	KLF1	Kruppel-like factor 1	0.0353	-0.0131	-0.2229	-0.0726	0.0907	101 ± 17	101 ± 12	101 ± 13	150 ± 25
219371_s_at	KLF2	Kruppel-like factor 2	0.2745	-0.0500	0.0070	-0.3375	0.0592	463 ± 36	681 ± 121	637 ± 46	800 ± 16
209212_s_at	KLF5	Kruppel-like factor 5	0.0384	-0.0386	-0.1339	-0.4130	0.0518	177 ± 14	156 ± 16	180 ± 6	230 ± 33
204334_at	KLF7	Kruppel-like factor 7	0.0029	-0.0743	0.0547	-0.0926	0.0601	664 ± 44	848 ± 69	759 ± 41	938 ± 22
205783_at	KLK13	kallikrein 13	0.0193	-0.0176	-0.0057	0.2616	0.0263	215 ± 14	215 ± 14	244 ± 29	314 ± 31
211519_s_at	KNLSL6	kinesin-like 6	0.1543	-0.0145	0.0785	-0.1533	0.0704	172 ± 19	193 ± 14	194 ± 12	261 ± 4
213741_s_at	KPNA1	karyopherin α 1	0.5022	-0.0144	-0.0111	-0.4726	0.0258	256 ± 20	212 ± 36	236 ± 19	318 ± 9
212102_s_at	KPNA6	karyopherin α 6	0.0086	-0.0289	-0.4737	0.2894	0.0758	126 ± 15	125 ± 16	139 ± 18	190 ± 25
213574_s_at	KPNB1	karyopherin β 1	0.0000	-0.0012	0.3691	-0.1867	0.0057	1480 ± 67	1471 ± 104	1672 ± 66	2060 ± 201
212829_s_at	KPNB2	karyopherin β 2	0.0002	-0.0090	0.1923	-0.0920	0.0304	2337 ± 359	2292 ± 235	4071 ± 573	5202 ± 1378
214715_x_at	KR18	KRAB zinc finger protein KR18	0.0463	-0.0301	0.0998	-0.0290	0.1052	1839 ± 257	1919 ± 186	3117 ± 562	2720 ± 558
200914_x_at	KTN1	kinesin 1	0.0042	-0.0029	0.0276	-0.0678	0.0151	1603 ± 117	1988 ± 199	2350 ± 166	2475 ± 279
204328_at	LAK-4P	expressed in activated T/LAK lymphocytes	0.0060	-0.0056	0.3675	-0.3177	0.0220	549 ± 58	562 ± 31	671 ± 84	966 ± 161
205116_at	LAMA2	laminin, α 2	0.0478	-0.0026	0.0191	-0.0749	0.0316	114 ± 10	149 ± 20	142 ± 7	214 ± 42
202202_s_at	LAMA4	laminin, α 4	0.0268	-0.1425	0.0188	-0.0851	0.2081	189 ± 23	243 ± 37	280 ± 26	251 ± 41
200771_at	LAMC1	laminin, γ 1	0.1222	-0.0088	-0.2206	-0.0491	0.2585	655 ± 58	659 ± 53	739 ± 48	831 ± 107
201553_s_at	LAMP1	lysosomal-associated membrane protein 1	0.0005	-0.0216	0.1481	-0.3812	0.0864	9662 ± 723	3480 ± 1002	12482 ± 987	5386 ± 3118
218816_at	LANO	LAP and no PDZ protein	0.2624	-0.0241	-0.0383	0.4164	0.2297	324 ± 55	277 ± 33	387 ± 63	425 ± 40
219813_at	LATS1	LATS, large tumor suppressor, homolog 1	0.0107	-0.0175	0.2652	0.4151	0.0291	76 ± 9	84 ± 7	87 ± 8	133 ± 25
204256_at	LCE	long-chain fatty-acyl elongase	0.0081	-0.0282	-0.3269	0.4712	0.0690	362 ± 12	311 ± 29	381 ± 29	420 ± 35
202068_s_at	LDLR	low density lipoprotein receptor	0.5777	-0.0036	-0.0779	-0.3718	0.0505	520 ± 65	480 ± 55	496 ± 32	735 ± 97
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.0871	-0.0053	0.3217	-0.0455	0.1730	249 ± 14	266 ± 32	308 ± 26	330 ± 40
200923_at	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.5752	-0.0076	-0.2317	0.4148	0.1643	944 ± 131	864 ± 76	1097 ± 81	1277 ± 184
203235_s_at	LGALS9	lectin, galactoside-binding, soluble, 9	0.0020	-0.0105	0.0543	-0.2117	0.0060	237 ± 15	260 ± 24	235 ± 21	366 ± 42
221670_s_at	LHX3	LIM homeobox protein 3	0.0357	-0.5179	-0.2224	0.1234	0.4417	360 ± 33	308 ± 37	348 ± 31	408 ± 61
205876_at	LIFR	leukemia inhibitory factor receptor	0.0020	-0.0629	-0.1000	0.1700	0.0824	87 ± 13	73 ± 11	92 ± 10	134 ± 27
207857_at	LILRA2	leukocyte IgG-like receptor, subfamily A, member 2	0.0418	-0.0039	0.1243	-0.4168	0.0360	137 ± 19	150 ± 25	172 ± 11	224 ± 24
218850_s_at	LIMD1	LIM domains containing 1	0.1138	-0.0460	0.1431	0.4449	0.0733	266 ± 30	334 ± 47	314 ± 26	441 ± 72
202193_at	LIMK2	LIM domain kinase 2	0.0058	-0.0005	0.3244	-0.0156	0.0096	207 ± 22	238 ± 20	360 ± 64	402 ± 47
220036_s_at	LIMR	lipocalin-interacting membrane receptor	0.0188	-0.0284	-0.0343	0.4145	0.0315	598 ± 33	501 ± 28	599 ± 56	759 ± 83
219181_at	LIPG	lipase, endothelial	0.0430	-0.0122	0.1300	0.3529	0.1010	165 ± 19	164 ± 10	205 ± 26	231 ± 21
203713_s_at	LLGL2	lethal giant larvae homolog 2	0.0211	-0.0174	-0.3217	-0.0773	0.1607	98 ± 14	93 ± 23	149 ± 20	161 ± 42
220132_s_at	LLT1	lectin-like NK cell receptor	0.4310	-0.0278	0.4441	0.1543	0.0318	46 ± 9	31 ± 5	53 ± 8	74 ± 12
203411_s_at	LMNA	lamin A/C	0.2624	-0.0137	-0.2059	0.4986	0.0897	377 ± 48	372 ± 22	443 ± 31	503 ± 44
203276_at	LMNB1	lamin B1	0.2466	-0.0084	-0.0865	-0.0733	0.0564	87 ± 21	79 ± 12	144 ± 18	124 ± 18

Web Table 5 (19)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
212714_at	c-Mpl binding protein	0.1719	-0.0230	-0.0951	-0.0881	0.2554	698 ± 37	718 ± 68	721 ± 36	881 ± 122
213779_at	putative emu1	0.0037	-0.1094	0.0041	-0.3719	0.2095	408 ± 27	537 ± 83	554 ± 41	642 ± 141
213089_at	integral membrane glycoprotein-like	0.1854	-0.0153	0.3178	0.2622	0.1533	897 ± 136	1043 ± 229	1225 ± 215	1683 ± 364
222056_s_at	CGI-105 protein	0.0112	-0.3071	0.1059	0.0967	0.2871	790 ± 32	810 ± 39	937 ± 74	1683 ± 364
222158_s_at	CGI-146 protein	-0.7592	-0.0061	0.4618	0.1225	0.1719	109 ± 10	83 ± 11	131 ± 25	165 ± 36
201871_s_at	ORF	0.1092	-0.0285	0.2605	-0.4529	0.1719	733 ± 50	792 ± 76	895 ± 85	930 ± 29
218258_at	RNA polymerase I 16 kDa subunit	0.3085	-0.0248	0.2509	0.1511	0.0554	632 ± 31	590 ± 38	609 ± 39	760 ± 66
221131_at	α-1,4-N-acetylglucosaminyltransferase	0.0548	-0.0012	-0.4697	-0.0502	0.0204	193 ± 15	210 ± 17	236 ± 22	280 ± 24
219114_at	g20 protein	0.0237	-0.2277	0.1830	-0.3992	0.2764	276 ± 8	255 ± 18	334 ± 20	333 ± 63
210389_x_at	δ-tubulin	0.0002	-0.0032	0.0480	-0.2489	0.0040	137 ± 12	193 ± 19	211 ± 21	240 ± 21
219863_at	cyclin-E binding protein 1	0.1006	0.0000	0.0916	-0.0333	0.0077	252 ± 17	323 ± 30	336 ± 23	461 ± 73
219999_at	VRK3 for vaccinia related kinase 3	0.0439	-0.0004	0.0261	-0.2779	0.0000	330 ± 14	418 ± 42	369 ± 26	581 ± 24
219167_at	Ris	0.0071	-0.0008	0.1168	-0.1557	0.0181	701 ± 104	896 ± 140	1271 ± 204	1390 ± 97
207785_s_at	H-2K binding factor-2	0.4535	-0.0452	-0.2753	-0.0126	0.5700	1311 ± 84	1359 ± 130	1500 ± 64	1460 ± 157
219590_x_at	CGI-30 protein	0.0095	-0.0163	0.0016	-0.1407	0.0243	743 ± 14	872 ± 58	863 ± 35	917 ± 42
65521_at	ubiquitin-conjugating enzyme HBUCE1	0.0890	-0.0262	0.4014	0.1929	0.0145	575 ± 38	589 ± 24	580 ± 33	794 ± 84
217842_at	CGI-74 protein	0.0059	-0.0279	0.0225	-0.2132	0.0411	470 ± 39	553 ± 52	525 ± 21	671 ± 73
204097_s_at	CGI-79 protein	0.0163	-0.0716	-0.1577	0.4835	0.1456	446 ± 31	414 ± 50	468 ± 24	647 ± 139
208549_x_at	prothymosin α14	0.0051	-0.0579	0.2755	-0.2466	0.1181	1488 ± 127	1929 ± 316	1702 ± 152	2455 ± 459
212294_at	G-protein γ-12 subunit	0.2331	-0.0123	-0.3488	-0.3390	0.1419	904 ± 80	944 ± 88	1131 ± 121	1225 ± 141
220371_s_at	calbin-chloride cotransporter-interacting protein	0.0319	-0.0168	0.1159	-0.3570	0.0280	324 ± 23	398 ± 50	371 ± 29	529 ± 78
219366_at	cell death regulator aven	0.0851	-0.0061	-0.2302	-0.4037	0.0684	181 ± 26	163 ± 29	184 ± 19	261 ± 17
219307_at	candidate tumor suppressor protein	0.4561	-0.0164	0.4711	0.1795	0.2024	169 ± 11	167 ± 15	188 ± 17	219 ± 29
209944_at	clones 23567 and 23775 zinc finger protein	0.0148	-0.1498	-0.2433	0.3261	0.1760	1702 ± 163	1657 ± 157	2121 ± 185	1959 ± 143
219165_at	PDZ-LIM protein mystique	0.0170	-0.0053	0.1108	-0.4421	0.0110	231 ± 34	193 ± 25	318 ± 34	328 ± 23
215271_at	hypothetical protein similar to tenascin-R	0.0431	-0.0792	0.0580	-0.1605	0.1295	94 ± 12	92 ± 9	111 ± 22	170 ± 43
212274_at	lipin 1	0.0003	-0.0016	0.0580	-0.2010	0.0060	674 ± 76	813 ± 98	1051 ± 98	1104 ± 93
203549_s_at	lipoprotein lipase	0.9821	-0.0368	-0.2533	-0.1094	0.1573	686 ± 74	741 ± 75	733 ± 79	943 ± 98
202822_at	LIM domain containing preferred translocation partner in lipoma	0.1662	-0.0049	-0.3185	-0.3853	0.1172	895 ± 100	961 ± 79	1095 ± 64	1259 ± 167
221640_s_at	leucine-rich and death domain containing	0.0006	-0.0957	0.4677	-0.2515	0.2483	153 ± 29	191 ± 30	256 ± 34	250 ± 71
201412_at	low density lipoprotein receptor-related protein 10	0.0118	-0.0002	0.2710	-0.4640	0.0106	801 ± 70	911 ± 86	1052 ± 78	1233 ± 120
219188_s_at	LRP16 protein	0.0014	-0.0067	-0.0644	0.2029	0.0161	285 ± 18	256 ± 36	303 ± 27	441 ± 68
212650_s_at	low density lipoprotein receptor-related protein 4	0.4666	-0.0341	-0.2210	0.4485	0.3438	1505 ± 191	1604 ± 171	1890 ± 175	2036 ± 359
34697_at	low density lipoprotein receptor-related protein 6	0.2235	-0.0220	0.2343	-0.3992	0.0137	224 ± 33	196 ± 30	351 ± 37	292 ± 21
201861_s_at	leucine rich repeat interacting protein 1	0.0024	-0.0143	0.4284	-0.3903	0.0507	341 ± 37	321 ± 20	384 ± 38	516 ± 81
220610_s_at	leucine rich repeat interacting protein 2	0.0105	-0.0587	-0.2315	0.3641	0.1545	232 ± 23	238 ± 35	314 ± 27	302 ± 42
90610_at	leucine-rich repeat protein, neuronal 1	0.0021	-0.0214	0.3330	0.1749	0.0649	458 ± 52	567 ± 128	653 ± 83	909 ± 191
202903_at	US snRNA-associated Sm-like protein	0.0173	-0.0519	0.0028	-0.0512	0.0217	109 ± 11	168 ± 20	162 ± 8	187 ± 30
211018_at	lanosterol synthase	0.2231	-0.0141	-0.0112	-0.1288	0.1810	115 ± 22	87 ± 15	149 ± 23	165 ± 39
204682_at	latent transforming growth factor β binding protein 2	0.0068	-0.0219	0.1621	-0.2944	0.0367	320 ± 32	415 ± 50	370 ± 22	529 ± 77
219922_s_at	latent transforming growth factor β binding protein 3	0.1899	-0.0014	0.4053	0.3169	0.0141	478 ± 41	399 ± 56	559 ± 49	844 ± 165
40093_at	Lutheran blood group	0.0267	-0.0749	0.2284	0.1117	0.1643	296 ± 24	293 ± 79	380 ± 41	440 ± 60

Web Table 5 (20)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
220044_x_at	LUC7A	cisplatin resistance-associated overexpressed protein	0.0825	-0.0013	-0.3827	-0.0459	0.0087	1293 ± 68	1283 ± 114	1646 ± 48	1523 ± 98
203412_at	LZTR1	leucine-zipper-like transcriptional regulator, 1	0.0046	-0.1107	0.3603	-0.4392	0.1602	714 ± 48	808 ± 89	823 ± 70	986 ± 124
210302_s_at	MAB21L2	mab-21-like 2	0.0025	0.0000	0.0734	-0.0369	0.0001	145 ± 11	188 ± 9	197 ± 16	258 ± 21
208634_s_at	MADF1	microtubule-actin crosslinking factor 1	0.1273	-0.0059	0.2891	-0.3500	0.1213	6029 ± 397	6370 ± 490	7020 ± 245	7661 ± 293
212346_s_at	MAD4	MAX dimerization protein 4	0.0010	-0.0265	0.3865	-0.2169	0.0819	389 ± 46	423 ± 24	507 ± 19	658 ± 144
208037_s_at	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	0.0275	-0.0619	0.1521	-0.4532	0.0180	315 ± 35	394 ± 66	311 ± 25	537 ± 78
203077_s_at	MADH2	MAD, mothers against decapentaplegic homolog 2	0.2862	-0.0368	-0.3903	-0.3001	0.3342	318 ± 14	306 ± 8	356 ± 23	355 ± 37
202526_at	MADH4	MAD, mothers against decapentaplegic homolog 4	-0.7954	-0.0096	0.0958	-0.1898	0.2556	92 ± 9	84 ± 7	108 ± 14	116 ± 13
205187_at	MADH5	MAD, mothers against decapentaplegic homolog 5	0.0081	-0.0343	0.1287	-0.1805	0.0319	53 ± 6	65 ± 12	97 ± 12	88 ± 12
218559_s_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B	0.2956	-0.0035	0.3005	0.1221	0.0128	407 ± 40	335 ± 25	412 ± 63	626 ± 80
36711_at	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F	0.1017	-0.0017	-0.1085	-0.2944	0.0421	702 ± 150	781 ± 178	1614 ± 423	1741 ± 363
204970_s_at	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G	0.0243	-0.0366	-0.2613	0.1171	0.0816	813 ± 111	608 ± 41	890 ± 49	1083 ± 191
206218_at	MAGEB2	melanoma antigen, family B, 2	0.0134	-0.0106	-0.4312	0.3334	0.0534	106 ± 13	96 ± 12	119 ± 6	170 ± 35
210017_at	MALT1	mucosa associated lymphoid tissue lymphoma transloc. 1	0.0422	-0.0071	-0.3718	-0.0078	0.0655	101 ± 12	118 ± 17	142 ± 9	145 ± 12
65884_at	MAN1B1	mannosidase, α, class 1B, member 1	0.0158	-0.2430	0.1404	-0.0781	0.2107	374 ± 26	395 ± 24	465 ± 22	424 ± 53
202032_s_at	MAN2A2	mannosidase, α, class 2A, member 2	0.5955	-0.0108	0.4182	-0.0852	0.1884	1141 ± 70	1242 ± 51	1307 ± 114	1463 ± 152
209166_s_at	MAN2B1	mannosidase, α, class 2B, member 1	0.0062	-0.0036	-0.4465	-0.1480	0.0134	288 ± 31	298 ± 60	328 ± 33	509 ± 70
202424_at	MAP2K2	mitogen-activated protein kinase kinase 2	0.0280	-0.0812	-0.4688	0.3035	0.3280	2156 ± 174	1988 ± 117	2579 ± 289	3084 ± 800
215498_s_at	MAP2K3	mitogen-activated protein kinase kinase 3	0.0000	-0.0003	0.1738	-0.1373	0.0016	207 ± 23	240 ± 27	319 ± 35	375 ± 28
216206_x_at	MAP2K7	mitogen-activated protein kinase kinase 7	0.0135	-0.0257	0.1166	-0.0778	0.0755	196 ± 25	197 ± 14	307 ± 43	292 ± 53
203652_at	MAP3K11	mitogen-activated protein kinase kinase kinase 11	0.0016	-0.0166	0.2092	0.3177	0.0530	704 ± 45	738 ± 87	863 ± 92	1180 ± 233
205192_at	MAP3K14	mitogen-activated protein kinase kinase kinase 14	0.0340	-0.0191	0.2121	-0.3673	0.1328	309 ± 42	367 ± 40	385 ± 33	480 ± 78
203514_at	MAP3K3	mitogen-activated protein kinase kinase kinase 3	0.0016	-0.0190	0.1606	-0.3785	0.0662	349 ± 29	414 ± 55	480 ± 26	540 ± 84
243_g_at	MAP4	microtubule-associated protein 4	0.0076	-0.1287	0.1900	-0.4409	0.2930	1991 ± 134	1954 ± 216	2538 ± 254	2367 ± 390
202890_at	MAP7	microtubule-associated protein 7	0.4108	-0.0418	-0.2125	-0.2200	0.3319	1664 ± 158	1720 ± 217	2051 ± 218	2005 ± 115
208351_s_at	MAPK1	mitogen-activated protein kinase 1	0.0028	-0.0084	-0.0824	0.0572	0.0053	212 ± 14	184 ± 12	226 ± 15	272 ± 20
206106_at	MAPK12	mitogen-activated protein kinase 12	0.0116	-0.1412	0.2112	-0.0892	0.2916	192 ± 21	238 ± 31	234 ± 16	298 ± 72
201460_at	MAPKAPK2	mitogen-activated protein kinase kinase-activated protein kinase 2	0.0088	-0.0414	0.1902	0.2897	0.0992	644 ± 44	761 ± 104	763 ± 80	940 ± 98
202569_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	0.0053	-0.0086	-0.2661	-0.1510	0.0082	364 ± 27	358 ± 14	466 ± 23	435 ± 25
206449_s_at	MASP1	mannan-binding lectin serine protease 1	-0.5137	-0.0187	0.2096	0.3410	0.0039	117 ± 8	105 ± 8	87 ± 13	171 ± 24
215903_s_at	MAST205	microtubule assoc. testis specific serine/threonine prot. kinase	0.0133	-0.0046	0.2525	-0.2152	0.0164	562 ± 48	503 ± 48	703 ± 47	780 ± 90
213705_at	MAT2A	methionine adenosyltransferase II, α	0.1291	-0.0001	0.0133	-0.0184	0.0038	316 ± 29	434 ± 58	490 ± 25	733 ± 137
203332_s_at	MAX	MAX protein	0.1427	-0.0007	0.0691	-0.0219	0.0266	377 ± 45	508 ± 59	471 ± 46	634 ± 76
212064_x_at	MAZ	MYC-associated zinc finger protein	0.0672	-0.0078	-0.1406	0.2432	0.0402	2796 ± 181	2330 ± 97	2988 ± 170	3381 ± 374
204179_at	MB	myoglobin	0.0249	-0.4632	-0.0091	0.3543	0.1634	1125 ± 75	1036 ± 57	1420 ± 97	1218 ± 206
41160_at	MBD3	methy-CpG binding domain protein 3	0.3415	-0.0084	-0.1165	0.2485	0.0711	198 ± 24	185 ± 8	224 ± 19	276 ± 37
210136_at	MBP	myelin basic protein	0.0124	-0.0232	0.2830	-0.3059	0.0881	1863 ± 130	1716 ± 106	2335 ± 218	2529 ± 404
205468_at	MC1R	melanocortin 1 receptor	0.0343	-0.0383	0.0285	-0.4138	0.2970	1624 ± 245	1962 ± 326	2352 ± 674	3195 ± 956
205716_at	MCFP	mitochondrial carrier family protein	0.2192	-0.0198	0.3825	0.4837	0.1997	212 ± 19	193 ± 23	261 ± 34	297 ± 57
214057_at	MCL1	myeloid cell leukemia sequence 1	0.7286	-0.0439	0.1984	0.2795	0.0938	138 ± 13	120 ± 8	129 ± 13	173 ± 19
208795_s_at	MCM7	MCM7 minichromosome maintenance deficient 7	0.0414	-0.0009	0.0519	-0.0378	0.0349	209 ± 16	232 ± 21	253 ± 29	314 ± 29
			0.0461	-0.2605	-0.1340	0.2613	0.5904	439 ± 69	431 ± 52	535 ± 72	545 ± 101

Web Table 5 (21)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
213761_at	MDM1	nuclear protein double minute 1	0.2852	-0.0016	0.0725	-0.0364	0.0135	315 ± 13	386 ± 26	389 ± 21	418 ± 25
213816_s_at	NET	met proto-oncogene	0.0087	-0.0686	0.0403	-0.2312	0.0995	136 ± 13	182 ± 30	168 ± 17	220 ± 32
203406_at	MFAP1	microfibrillar-associated protein 1	0.0001	-0.0001	0.0005	-0.0454	0.0004	877 ± 21	956 ± 44	1096 ± 20	1117 ± 58
201126_s_at	MGAT1	mannosyl-glycoprotein β-1,2-N-acetylglucosaminyltransferase	0.0216	-0.1793	0.2577	-0.4527	0.3490	573 ± 43	603 ± 45	682 ± 46	677 ± 73
209497_s_at	MGC10871	hypothetical protein similar to RNA-binding protein lark	0.0324	-0.3426	-0.4598	0.3893	0.4320	601 ± 85	758 ± 106	710 ± 73	813 ± 119
64408_s_at	MGC4809	serologically defined breast cancer antigen NY-BR-20	0.0288	-0.0786	-0.4929	-0.0433	0.2675	65 ± 9	64 ± 9	89 ± 17	92 ± 14
205905_s_at	MICA	MHC class I polypeptide-related sequence A	0.0711	-0.0399	0.1274	-0.4064	0.1107	155 ± 13	180 ± 23	176 ± 19	261 ± 59
206247_at	MICB	MHC class I polypeptide-related sequence B	0.0038	-0.0005	0.1496	-0.1426	0.0044	138 ± 10	122 ± 5	192 ± 27	281 ± 52
210694_s_at	MID1	midline 1	0.0751	-0.0048	-0.4117	-0.1303	0.0584	370 ± 40	422 ± 64	414 ± 29	577 ± 78
207233_s_at	MITF	microphthalmia-associated transcription factor	0.0224	-0.0609	0.1805	-0.2943	0.1083	407 ± 48	554 ± 66	537 ± 52	637 ± 96
218205_s_at	MKNK2	MAP kinase-interacting serine/threonine kinase 2	0.0001	-0.0058	0.3211	-0.3921	0.0601	1676 ± 152	1789 ± 282	2409 ± 305	2758 ± 148
218845_at	MKPX	mitogen-activated protein kinase phosphatase x	0.0038	-0.0282	0.3287	0.2653	0.0136	1014 ± 42	1014 ± 93	1046 ± 53	1457 ± 183
201285_at	MKRN1	makorin, ring finger protein, 1	0.2066	-0.0168	-0.1629	-0.4398	0.2428	1013 ± 33	1016 ± 51	1106 ± 36	1121 ± 65
208082_x_at	MKRN4	makorin, ring finger protein, 4	0.0259	-0.3632	0.2007	-0.1776	0.0991	900 ± 92	977 ± 114	1336 ± 126	1017 ± 88
206426_at	MLANA	melan-A	0.0053	-0.0574	0.0085	-0.3347	0.2505	57 ± 6	72 ± 14	83 ± 10	104 ± 27
213395_at	MLC1	megakaryocytic leukoencephalopathy with subcortical cysts 1	0.0201	-0.1278	0.1608	-0.3273	0.0755	1076 ± 142	1294 ± 213	1793 ± 138	1416 ± 288
201924_at	MLL T2	myeloid/lymphoid or mixed-lineage leukemia	0.0089	-0.0009	-0.3971	0.3371	0.0224	1667 ± 128	1606 ± 134	2181 ± 213	2576 ± 399
207842_s_at	MLN51	MLN51 protein	0.0036	-0.0007	0.2351	-0.0527	0.0062	1372 ± 115	1647 ± 183	2258 ± 256	2199 ± 212
204580_at	MMP12	matrix metalloproteinase 12	-0.9509	-0.0303	0.1792	0.2065	0.0077	116 ± 12	100 ± 9	99 ± 7	163 ± 19
207012_at	MMP16	matrix metalloproteinase 16	0.7754	-0.0464	0.1365	-0.1226	0.2746	100 ± 9	98 ± 8	114 ± 10	131 ± 21
201069_at	MMP2	matrix metalloproteinase 2	0.0807	-0.0240	0.1786	-0.3588	0.0292	242 ± 30	327 ± 49	268 ± 24	419 ± 62
220201_at	MNAB	membrane-associated nucleic acid binding protein	0.5089	-0.0365	-0.2946	0.1330	0.0309	143 ± 15	95 ± 20	146 ± 20	195 ± 28
212462_at	MORF	monocytic leukemia zinc finger protein-related factor	0.0042	-0.0079	0.4942	-0.3379	0.0143	803 ± 53	805 ± 25	982 ± 41	1075 ± 104
203524_s_at	MPST	mercaptopyruvate sulfoxidase	0.0052	-0.0287	-0.1137	0.1436	0.0278	580 ± 61	565 ± 45	603 ± 78	875 ± 108
206538_at	MRAS	muscle RAS oncogene homolog	0.0163	-0.7755	0.4340	0.2705	0.2830	152 ± 29	208 ± 43	243 ± 29	203 ± 36
221995_s_at	MRP63	mitochondrial ribosomal protein 63	0.0236	-0.0306	0.0945	0.4858	0.0078	234 ± 20	296 ± 32	249 ± 8	434 ± 74
41220_at	MSF	MLL septin-like fusion	0.0201	-0.0019	0.1894	0.4429	0.0079	3652 ± 302	3381 ± 172	4726 ± 414	5008 ± 399
210533_at	MSH4	mutS homolog 4	0.0428	-0.0565	-0.1952	-0.0760	0.1417	112 ± 11	116 ± 13	109 ± 12	173 ± 39
205832_s_at	MSX1	nsh homeo box homolog 1	0.0189	-0.0007	0.2089	-0.1222	0.0141	596 ± 38	676 ± 106	778 ± 61	1163 ± 229
206461_x_at	MT1H	metallothionein 1H	0.4224	-0.0184	-0.4401	-0.1084	0.1491	7403 ± 686	8572 ± 632	8638 ± 906	9388 ± 1269
204326_x_at	MT1L	metallothionein 1L	0.1130	-0.0139	0.4215	-0.1706	0.0272	6290 ± 635	7881 ± 601	7372 ± 890	9500 ± 318
208581_x_at	MT1X	metallothionein 1X	0.7046	-0.0358	-0.2987	-0.1080	0.1314	6620 ± 1243	12186 ± 687	1168 ± 1145	4632 ± 1617
212185_x_at	MT2A	metallothionein 2A	0.6080	-0.0283	-0.3102	-0.2349	0.1771	7870 ± 2129	9802 ± 1006	1101 ± 1397	3863 ± 2800
211783_s_at	MTA1	metastasis associated 1	0.0495	-0.0048	-0.4272	0.2196	0.0022	917 ± 50	837 ± 17	944 ± 68	1368 ± 167
205323_s_at	MTF1	metal regulatory transcription factor 1	0.0336	-0.0001	0.2922	-0.0566	0.0111	419 ± 32	476 ± 32	538 ± 22	570 ± 43
203433_at	MTHFS	5,10-methylenetetrahydrofolate synthetase	0.0063	-0.1228	0.2313	-0.0677	0.4588	260 ± 33	242 ± 53	274 ± 58	355 ± 63
203095_at	MTIF2	mitochondrial translational initiation factor 2	0.0002	-0.0065	0.0930	-0.2917	0.0418	411 ± 31	418 ± 35	522 ± 44	575 ± 63
207847_s_at	MUC1	mucin 1, transmembrane	0.0790	-0.0180	0.4843	0.3841	0.0227	254 ± 29	263 ± 35	267 ± 14	414 ± 64
217117_x_at	MUC3A	mucin 3A, intestinal	0.2290	-0.0012	0.0708	-0.0535	0.0234	411 ± 27	448 ± 40	480 ± 53	645 ± 77
207727_s_at	MUTYH	mutY homolog	0.0200	-0.0354	0.4997	0.4970	0.1024	634 ± 69	753 ± 92	729 ± 39	910 ± 99
36907_at	MVK	mevalonate kinase	0.0798	-0.0020	0.3448	0.4876	0.0052	1115 ± 24	1287 ± 95	1265 ± 96	1610 ± 105
204994_at	MX2	myxovirus resistance 2	0.5644	-0.0276	0.2472	-0.2149	0.1845	289 ± 25	311 ± 30	290 ± 26	432 ± 99

Web Table 5 (22)

Probe set	Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
202364_at	MX11	MAX interacting protein 1	0.0543	-0.0153	-0.0209	-0.3737	0.1029	4690 ± 458	4852 ± 492	5951 ± 413	5997 ± 504
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog -like 1	0.0637	-0.0039	0.3402	-0.1240	0.0618	172 ± 15	197 ± 16	249 ± 36	245 ± 14
214087_s_at	MYBPC1	myosin binding protein C, slow type	0.1441	-0.0324	-0.2576	-0.3289	0.1974	1473 ± 271	1384 ± 106	2123 ± 249	2011 ± 441
209757_s_at	MYCN	v-myc myelocytomatosis viral related oncogene	0.1525	-0.0008	0.4780	-0.1110	0.0260	113 ± 12	130 ± 22	166 ± 17	180 ± 12
217274_x_at	MYL4	myosin, light polypeptide 4, alkali; atrial, embryonic	0.0416	-0.0287	0.3234	-0.2108	0.0551	220 ± 15	212 ± 10	227 ± 14	337 ± 68
202555_s_at	MYLK	myosin, light polypeptide kinase	0.0195	-0.0367	0.2422	-0.1911	0.1238	788 ± 87	970 ± 98	985 ± 124	1151 ± 104
201976_s_at	MYO10	myosin X	0.0988	-0.0457	0.0290	-0.2051	0.1025	3064 ± 290	3944 ± 556	4474 ± 301	4214 ± 576
59375_at	MYO15BP	myosin XVb pseudogene	0.0454	-0.2505	0.1104	0.4554	0.1478	560 ± 46	703 ± 99	528 ± 39	865 ± 200
21916_s_at	MYO1A	myosin IA	0.0123	-0.0142	-0.3886	-0.0494	0.0495	214 ± 13	229 ± 20	240 ± 13	314 ± 45
32811_at	MYO1C	myosin IC	0.2342	-0.0186	0.3034	-0.3232	0.0939	1185 ± 113	1162 ± 118	1272 ± 35	1621 ± 113
203072_at	MYO1E	myosin IE	0.1401	-0.0248	0.2110	-0.0881	0.0100	175 ± 22	239 ± 14	187 ± 17	264 ± 23
212687_at	MYO1F	myosin IF	0.0775	0.0000	-0.1813	-0.2269	0.0012	2144 ± 409	2016 ± 262	3497 ± 590	5316 ± 867
218966_at	MYO5C	myosin 5C	0.0277	-0.0019	0.2926	-0.3093	0.0052	512 ± 35	624 ± 61	579 ± 47	816 ± 83
203215_s_at	MYO6	myosin VI	0.0181	-0.2041	0.1624	-0.0700	0.3753	158 ± 40	217 ± 49	202 ± 30	323 ± 26
214780_s_at	MYO9B	myosin IXb	0.0028	-0.0088	0.1093	-0.3535	0.0218	480 ± 33	647 ± 68	738 ± 69	837 ± 19
205610_at	MYOM1	myomesin 1 185kDa	0.0003	-0.0017	0.3562	-0.0983	0.0161	85 ± 21	101 ± 16	179 ± 23	198 ± 46
32069_at	NABP1	Nedd4 binding protein 1	0.0019	-0.0011	-0.0369	-0.4043	0.0073	327 ± 27	309 ± 42	374 ± 26	470 ± 20
207196_s_at	NAF1	Nef-associated factor 1	0.0067	-0.0010	0.0764	-0.0589	0.0063	465 ± 33	520 ± 39	633 ± 35	656 ± 59
202926_at	NAG	neuroblastoma-amplified protein	0.0038	-0.0877	0.0297	-0.1395	0.1210	589 ± 40	749 ± 55	715 ± 60	787 ± 89
202943_s_at	NAGA	N-acetylgalactosaminidase, α-	0.2581	-0.0058	0.2561	-0.3471	0.0625	403 ± 31	424 ± 25	433 ± 23	526 ± 46
218084_s_at	NAPAP95	neighbor of A-kinase anchoring protein 95	0.0589	-0.0073	-0.1590	0.0080	0.0038	772 ± 59	600 ± 55	859 ± 67	1579 ± 343
204528_s_at	NAP1L1	nucleosome assembly protein 1-like 1	0.0216	-0.0102	0.3438	-0.0016	0.1583	1207 ± 78	1335 ± 97	1497 ± 134	1493 ± 107
201414_s_at	NAP1L4	nucleosome assembly protein 1-like 4	0.0326	-0.2180	0.1773	0.4221	0.2869	919 ± 56	967 ± 94	1116 ± 44	1047 ± 116
218330_s_at	NAV2	neuron navigator 2	0.2265	-0.0010	-0.2585	-0.0533	0.0268	891 ± 93	972 ± 72	1264 ± 119	1392 ± 199
201913_s_at	NBP	nucleotide binding protein	0.2950	-0.0249	0.0855	-0.0581	0.3742	815 ± 57	869 ± 76	961 ± 143	1087 ± 140
212843_at	NCAM1	neural cell adhesion molecule 1	0.0080	-0.0607	-0.4805	0.2158	0.1489	4141 ± 191	4068 ± 411	4850 ± 375	5222 ± 565
211083_s_at	NCK1	NCK adaptor protein 1	0.0501	-0.0283	-0.4487	0.2968	0.0891	655 ± 25	566 ± 20	749 ± 71	735 ± 64
209061_at	NCOA3	nuclear receptor coactivator 3	0.2199	-0.0442	0.3014	-0.0053	0.1038	166 ± 24	218 ± 19	226 ± 12	279 ± 54
207760_s_at	NCOR2	nuclear receptor co-repressor 2	0.0007	-0.0205	0.3161	0.1962	0.0084	2231 ± 141	2095 ± 171	2767 ± 139	2938 ± 277
208759_at	NCSTN	nicastrin	0.0022	-0.0148	0.2609	0.3984	0.0215	604 ± 28	646 ± 50	620 ± 30	783 ± 54
202607_at	NDST1	N-deacetylase/N-sulfotransferase 1	0.0605	-0.0342	-0.4743	-0.0392	0.0542	499 ± 57	560 ± 55	761 ± 37	644 ± 102
203961_at	NEBL	nebulette	0.0496	-0.0037	-0.4161	-0.0204	0.0710	5126 ± 259	5476 ± 442	6672 ± 660	7214 ± 975
200015_s_at	NEED5	neural precursor expressed, developmentally down-regulated	0.1540	-0.0053	0.1331	-0.0581	0.0533	3651 ± 234	4068 ± 399	4858 ± 186	4833 ± 458
219396_s_at	NEIL1	nei endonuclease VIII-like 1	0.0301	-0.1547	-0.1070	0.3798	0.2915	331 ± 47	336 ± 78	402 ± 30	476 ± 77
213328_at	NEK1	NIMA-related kinase 1	0.0326	-0.1439	0.1019	-0.0865	0.0632	210 ± 28	296 ± 30	301 ± 21	281 ± 27
212530_at	NEK7	NIMA-related kinase 7	0.0951	-0.0185	0.3140	-0.0241	0.2232	1295 ± 132	1424 ± 170	1790 ± 261	1687 ± 165
212299_at	NEK9	NIMA-related kinase 9	0.0231	-0.0037	-0.0972	-0.0904	0.1022	671 ± 58	704 ± 101	786 ± 65	933 ± 87
206948_at	NEU3	sialidase 3	0.0481	-0.0903	-0.3657	0.3676	0.0150	204 ± 11	200 ± 28	165 ± 25	316 ± 55
214799_at	NFASC	neurofascin	0.0403	-0.0143	0.2598	-0.1212	0.0612	927 ± 155	1373 ± 236	1897 ± 324	1733 ± 352
211105_s_at	NFATC1	nuclear factor of activated T-cells, calcineurin-dependent 1	0.0244	-0.0010	-0.4702	-0.2771	0.0178	284 ± 29	294 ± 39	316 ± 25	502 ± 93
207416_s_at	NFATC3	nuclear factor of activated T-cells, calcineurin-dependent 3	0.2278	-0.0205	0.4054	-0.4599	0.1522	159 ± 20	168 ± 24	209 ± 28	225 ± 10
200759_x_at	NFE2L1	nuclear factor -like 1	0.0002	-0.0083	-0.1371	0.1569	0.0449	3717 ± 135	3695 ± 357	4159 ± 99	4798 ± 473

Web Table 5 (23)

WO 2005/076939			PCT/US2005/003668									
Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe	
204702_s_at	NFE2L3	nuclear factor-like 3	0.0981	-0.0338	0.1887	-0.2065	0.0478	81 ± 10	101 ± 8	95 ± 9	136 ± 22	
209289_at	NFIB	nuclear factor I/B	0.0751	-0.0266	0.1744	0.3378	0.1231	2449 ± 153	2587 ± 188	2843 ± 141	3078 ± 286	
213298_at	NFIC	nuclear factor I/C	0.0026	-0.0056	0.0037	-0.0541	0.0127	126 ± 10	158 ± 14	180 ± 8	234 ± 40	
209239_at	NFKB1	NFκ light polypeptide gene enhancer in B-cells 1	0.0219	-0.3815	-0.3905	-0.3749	0.6568	458 ± 33	500 ± 42	493 ± 36	532 ± 59	
201502_s_at	NFKBIA	NFκ light polypeptide gene enhancer in B-cells inhibitor, α	0.0057	-0.0041	-0.2975	-0.2235	0.0073	1776 ± 294	1999 ± 377	2682 ± 493	4203 ± 735	
210268_at	NFX1	nuclear transcription factor, X-box binding 1	0.0026	-0.0222	0.1403	-0.0758	0.0635	76 ± 14	112 ± 21	143 ± 23	148 ± 25	
202008_s_at	NID	nidogen	0.2302	-0.0339	0.1322	-0.1095	0.0045	133 ± 8	204 ± 23	142 ± 12	230 ± 32	
215338_s_at	NKTR	natural killer-tumor recognition sequence	0.0129	-0.1353	0.0301	-0.2544	0.0117	181 ± 13	225 ± 27	292 ± 21	234 ± 28	
217844_at	NLI1F	nuclear LIM interactor-interacting factor	0.0141	-0.0102	0.0314	-0.0301	0.0436	630 ± 92	791 ± 83	1116 ± 90	1117 ± 258	
205204_at	NMB	neuromedin B	0.0007	-0.0059	0.0169	0.4550	0.0383	432 ± 33	482 ± 62	492 ± 42	737 ± 39	
204862_s_at	NME3	non-melanistic cells 3, protein expressed in	0.0016	-0.0005	0.4648	-0.1352	0.0022	548 ± 38	582 ± 72	612 ± 22	914 ± 109	
212739_s_at	NME4	non-melanistic cells 4, protein expressed in	0.0080	-0.0083	0.0959	-0.2639	0.0036	750 ± 43	692 ± 72	1036 ± 68	952 ± 81	
202237_at	NNMT	nicotinamide N-methyltransferase	0.0773	-0.0235	-0.2385	0.1065	0.0010	201 ± 27	89 ± 20	147 ± 22	308 ± 46	
214427_at	NOL1	nucleolar protein 1, 120kDa	0.0218	-0.2247	-0.1073	0.2250	0.3489	850 ± 66	796 ± 116	868 ± 80	1053 ± 43	
200874_s_at	NOL5A	nucleolar protein 5A	0.0194	-0.0054	-0.0087	0.0914	0.0318	305 ± 13	272 ± 7	349 ± 38	395 ± 37	
200057_s_at	NONO	non-POU domain containing, octamer-binding	0.0360	-0.0029	-0.4987	-0.0379	0.0445	3672 ± 99	3873 ± 104	4017 ± 165	4172 ± 110	
217950_at	NOSIP	eNOS interacting protein	0.0205	-0.1487	-0.1308	0.0772	0.4777	502 ± 41	484 ± 26	553 ± 62	605 ± 88	
205247_at	NOTCH4	Notch homolog 4	0.1144	-0.0163	0.0020	0.4330	0.0348	302 ± 17	360 ± 40	367 ± 28	474 ± 62	
220316_at	NPAS3	basic-helix-loop-helix-PAS protein	0.0759	-0.0001	0.0029	-0.1486	0.0011	427 ± 16	554 ± 44	617 ± 17	796 ± 108	
202679_at	NPC1	Niemann-Pick disease, type C1	-0.6334	-0.0085	-0.2478	-0.3528	0.2017	1188 ± 120	1093 ± 103	1197 ± 118	1503 ± 168	
215090_x_at	NPEPPS	aminopeptidase puromycin sensitive	0.0244	-0.0310	-0.0994	-0.2947	0.2896	681 ± 46	704 ± 75	761 ± 48	822 ± 51	
217041_at	NPTXR	neuronal pentrexin receptor	0.9277	-0.0482	-0.2217	-0.4873	0.3205	208 ± 20	207 ± 21	238 ± 18	273 ± 47	
3131637_s_at	NR1D1	nuclear receptor subfamily 1, group D, member 1	0.0110	-0.4574	-0.3669	0.4310	0.4949	2771 ± 256	3307 ± 583	2925 ± 490	3686 ± 491	
209506_s_at	NR2F1	nuclear receptor subfamily 2, group F, member 1	0.0289	-0.2429	0.1921	-0.0775	0.8210	542 ± 23	568 ± 23	596 ± 54	619 ± 106	
209262_s_at	NR2F6	nuclear receptor subfamily 2, group F, member 6	0.0482	-0.0951	-0.4242	0.0542	0.0882	436 ± 32	408 ± 63	418 ± 32	613 ± 98	
216979_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	0.2152	-0.0037	0.0524	-0.2079	0.0265	86 ± 7	88 ± 12	104 ± 12	150 ± 26	
2124632_at	NRP2	neuropilin 2	0.0498	-0.0981	-0.1788	-0.4201	0.1182	127 ± 14	86 ± 17	120 ± 12	145 ± 21	
209982_s_at	NRXN2	neurexin 2	0.0111	-0.2299	-0.4993	-0.3509	0.2346	488 ± 41	542 ± 54	605 ± 48	677 ± 108	
203718_at	NTE	neuropathy target esterase	0.0077	-0.7111	0.4995	-0.4016	0.9043	1308 ± 102	1387 ± 157	1466 ± 187	1459 ± 259	
217033_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.0020	-0.0579	0.1423	0.4117	0.0866	806 ± 38	897 ± 106	1029 ± 81	1098 ± 102	
217802_s_at	NUCKS	similar to rat nuclear ubiquitous casein kinase 2	0.0001	-0.0002	0.0099	-0.1530	0.0013	4406 ± 107	4549 ± 104	5193 ± 244	5660 ± 313	
21210574_s_at	NUDC	nuclear distribution gene C homolog	0.0143	-0.6804	0.4860	0.3653	0.4315	1192 ± 56	1181 ± 70	1343 ± 67	1201 ± 118	
21218414_s_at	NUDE1	LIS1-interacting protein NUDE1, rat homolog	0.0039	-0.0333	0.2772	0.4052	0.1041	667 ± 108	780 ± 187	994 ± 161	1401 ± 366	
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	0.0008	-0.0052	0.2004	-0.0377	0.0547	740 ± 72	879 ± 74	987 ± 66	1133 ± 170	
207545_s_at	NUMB	numb homolog	0.3200	-0.0075	0.2505	-0.0534	0.0465	120 ± 8	119 ± 17	168 ± 17	167 ± 20	
2121709_at	NUP160	nucleoporin 160kDa	0.0067	-0.0001	0.4503	-0.0642	0.0004	151 ± 11	185 ± 12	213 ± 16	245 ± 11	
202155_s_at	NUP214	nucleoporin 214kDa	0.0128	-0.0011	-0.4361	-0.0709	0.0094	390 ± 24	401 ± 44	445 ± 20	536 ± 33	
219007_at	Nup43	nucleoporin Nup43	0.0636	-0.0199	0.1865	-0.3225	0.0635	539 ± 55	572 ± 39	710 ± 47	738 ± 92	
203195_s_at	NUP98	nucleoporin 98kDa	0.0044	-0.0001	0.1507	-0.0104	0.0000	97 ± 10	154 ± 25	250 ± 12	233 ± 27	
203195_s_at	NYX	nyctalopin	0.0154	-0.0634	0.0984	-0.2008	0.1515	98 ± 14	117 ± 10	125 ± 9	180 ± 48	
221684_s_at	OASL	2'-5'-oligoadenylate synthetase-like	0.3167	-0.0139	0.1112	-0.0072	0.1729	282 ± 34	335 ± 19	332 ± 25	399 ± 55	
210797_s_at	ODC1	ornithine decarboxylase 1	0.1019	-0.0166	0.4136	-0.3532	0.0544	948 ± 48	879 ± 53	864 ± 35	1217 ± 176	

Web Table 5 (24)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
203568_s_at	OFD1	oral-facial-digital syndrome 1	0.0071	-0.0016	-0.3908	-0.1424	0.0326	1060 ± 101	1179 ± 94	1411 ± 124	1546 ± 159
201282_at	OGDH	oxoglutarate dehydrogenase	0.0460	-0.9567	-0.2534	0.3984	0.0340	622 ± 72	623 ± 88	924 ± 73	586 ± 118
205301_s_at	OGG1	8-oxoguanine DNA glycosylase	0.1250	-0.0181	0.1970	-0.0363	0.0777	57 ± 7	71 ± 7	108 ± 20	103 ± 22
215136_s_at	OIP2	Opa-interacting protein 2	0.0322	-0.0077	0.0628	-0.1313	0.0200	267 ± 10	355 ± 36	334 ± 22	419 ± 50
205323_s_at	OPHN1	oligophrenin 1	0.0084	-0.0069	0.1390	-0.3364	0.0301	2393 ± 277	2949 ± 391	3086 ± 78	4482 ± 876
221460_at	OR2C1	olfactory receptor, family 2, subfamily C, member 1	0.0335	-0.0144	-0.4954	0.3644	0.0770	283 ± 40	259 ± 21	322 ± 47	465 ± 94
215770_at	OR7E2P	olfactory receptor, 7E2	0.5560	-0.0046	-0.0931	0.2537	0.0094	45 ± 6	30 ± 6	42 ± 13	86 ± 15
207408_at	ORCTL4	organic cationic transporter-like 4	0.0328	-0.0168	-0.0380	0.3543	0.0312	350 ± 25	337 ± 23	365 ± 30	506 ± 72
208735_s_at	OS4	conserved gene amplified in osteosarcoma	0.0542	-0.0290	0.0126	0.3074	0.0849	450 ± 25	483 ± 50	496 ± 27	605 ± 61
215399_s_at	OS-9	amplified in osteosarcoma	0.0037	-0.4339	0.0377	0.2597	0.4182	355 ± 24	395 ± 47	437 ± 20	415 ± 56
218304_s_at	OSBP11	oxysterol binding protein-like 11	0.2868	-0.0153	-0.3162	-0.0412	0.2455	704 ± 69	837 ± 129	961 ± 110	993 ± 146
213039_at	P114-RHO-GEF	Rho-specific guanine nucleotide exchange factor p114	0.1011	-0.0312	-0.4892	0.0337	0.0606	1073 ± 35	1126 ± 163	1129 ± 81	1493 ± 150
202553_s_at	P29	GCIP-interacting protein p29	0.0025	-0.0574	0.1144	-0.0131	0.0550	998 ± 90	1164 ± 72	1308 ± 75	1189 ± 66
220408_x_at	P38IP	transcription factor	0.0884	-0.0190	-0.4874	-0.3214	0.0123	743 ± 68	763 ± 99	729 ± 49	1063 ± 44
220402_at	P53AIP1	p53-regulated apoptosis-inducing protein 1	0.0912	-0.0004	0.0885	-0.0401	0.0000	47 ± 9	57 ± 7	43 ± 8	124 ± 16
220406_at	P84	nuclear matrix protein p84	0.0263	-0.1264	-0.2149	0.4118	0.1330	917 ± 91	917 ± 73	1180 ± 78	1041 ± 109
212220_at	PA200	proteasome activator 200 kDa	0.0035	-0.0876	0.0521	-0.2896	0.3204	77 ± 6	87 ± 16	105 ± 13	126 ± 34
215157_x_at	PABPC1	poly binding protein, cytoplasmic 1	0.0234	-0.0318	0.1606	-0.0525	0.1582	3495 ± 151	3731 ± 242	4100 ± 273	4097 ± 223
208113_x_at	PABPC3	poly binding protein, cytoplasmic 3	0.0287	-0.1967	0.0367	-0.0759	0.3436	2272 ± 174	2625 ± 405	2907 ± 234	2622 ± 145
201544_x_at	PABPN1	poly binding protein, nuclear 1	0.0060	-0.1873	0.4933	0.1838	0.2529	4230 ± 288	4405 ± 488	4544 ± 448	5912 ± 1094
201651_s_at	PACIN2	protein kinase C and casein kinase substrate in neurons 2	0.1415	-0.0026	-0.1714	0.0380	0.0178	2223 ± 156	1874 ± 170	2533 ± 133	3396 ± 579
205719_s_at	PAH	phenylalanine hydroxylase	0.4106	-0.0367	0.1758	-0.0028	0.3914	99 ± 13	120 ± 18	121 ± 8	128 ± 6
208878_s_at	PAK2	p21-activated kinase 2	0.4320	-0.0374	0.3637	-0.0987	0.1148	305 ± 24	363 ± 38	311 ± 18	408 ± 47
33814_at	PAK4	p21-activated kinase 4	0.0089	-0.0114	0.1352	-0.0533	0.0807	600 ± 39	625 ± 41	722 ± 44	847 ± 128
205815_at	PAP	pancreatitis-associated protein	0.0883	-0.0061	0.0663	-0.2791	0.0332	130 ± 10	171 ± 16	156 ± 13	221 ± 36
221527_s_at	PARD3	par-3 partitioning defective 3 homolog	0.0117	-0.0031	0.3044	-0.4089	0.0163	390 ± 40	350 ± 29	543 ± 60	563 ± 64
204004_at	PAWR	PRKC, apoptosis, WT1, regulator	0.2839	-0.0029	-0.2074	-0.0971	0.0977	274 ± 32	279 ± 33	330 ± 27	376 ± 32
205646_s_at	PAX6	paired box gene 6	0.0003	0.0000	0.2655	-0.1912	0.0024	1018 ± 115	1011 ± 98	1441 ± 189	2040 ± 299
220355_s_at	PB1	polybromo 1	0.0209	-0.0348	0.0362	-0.0008	0.0027	563 ± 20	639 ± 38	746 ± 32	650 ± 34
217739_s_at	PBEF	pre-B-cell colony-enhancing factor	0.5430	-0.0205	0.3250	-0.0138	0.2467	371 ± 34	411 ± 44	489 ± 58	499 ± 65
211097_s_at	PBX2	pre-B-cell leukemia transcription factor 2	0.0481	-0.0013	-0.4044	0.3876	0.0127	164 ± 11	143 ± 18	197 ± 14	225 ± 24
204476_s_at	PC	pyruvate carboxylase	0.0001	-0.0409	0.0223	-0.4650	0.1148	501 ± 40	596 ± 65	695 ± 67	713 ± 92
203845_at	PCAF	p300/CBP-associated factor	0.1777	-0.0450	0.0483	-0.0071	0.0645	112 ± 8	141 ± 21	125 ± 20	198 ± 36
217049_x_at	PCDH11Y	protocadherin 11 Y-linked	0.0178	-0.1013	0.0796	-0.4762	0.2160	2305 ± 195	2450 ± 219	2921 ± 243	2876 ± 341
205656_at	PCDH17	protocadherin 17	0.0769	-0.0190	0.4993	-0.1118	0.1086	2250 ± 176	2345 ± 232	2846 ± 205	2706 ± 160
219730_s_at	PCDH9	protocadherin 9	0.0943	-0.0377	-0.0541	0.3869	0.1044	1313 ± 127	1299 ± 70	1282 ± 85	1636 ± 130
214118_x_at	PCM1	pericentriolar material 1	0.0036	-0.6778	0.4751	0.4852	0.3157	580 ± 36	520 ± 68	708 ± 59	586 ± 115
201933_at	PCOLN3	procollagen N-endopeptidase	0.0025	-0.0129	-0.0647	0.3272	0.0039	180 ± 23	127 ± 17	238 ± 24	247 ± 25
205559_s_at	PCSK5	proprotein convertase subtilisin/kexin type 5	0.0001	-0.0014	0.0070	-0.0042	0.0029	174 ± 14	234 ± 16	313 ± 33	296 ± 36
212594_at	PCDC4	programmed cell death 4	0.0431	-0.3051	0.0069	-0.0113	0.0421	175 ± 21	204 ± 11	271 ± 28	204 ± 28
204449_at	PDCL	phosducin-like	0.0009	-0.0029	0.0846	-0.1842	0.0257	133 ± 8	141 ± 16	165 ± 26	234 ± 36
206388_at	PDE3A	phosphodiesterase 3A, cGMP-inhibited									

Web Table 5 (25)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
206792_x_at PDE4C	phosphodiesterase 4C, cAMP-specific	0.0069	-0.0180	0.0220	-0.1432	0.0466	4935 ± 632	3755 ± 1121	1049 ± 1345	8316 ± 1212
210836_x_at PDE4D	phosphodiesterase 4D, cAMP-specific	0.0374	-0.0467	-0.0044	0.4461	0.0851	108 ± 13	79 ± 17	106 ± 11	153 ± 31
216061_x_at PDGFB	platelet-derived growth factor β polypeptide	0.1198	-0.0065	0.0075	-0.0086	0.1059	376 ± 20	423 ± 60	550 ± 46	531 ± 96
202273_at PDGFRB	platelet-derived growth factor receptor, β polypeptide	0.0221	-0.0721	0.1187	-0.1005	0.0888	242 ± 26	334 ± 48	345 ± 24	346 ± 31
205137_x_at PDZ-73	PDZ-73 protein	0.0449	0.0000	0.1158	-0.0100	0.0004	219 ± 34	300 ± 64	385 ± 32	565 ± 65
208982_at PECAM1	platelet/endothelial cell adhesion molecule	0.0355	-0.0058	0.4207	-0.0699	0.1173	519 ± 62	516 ± 49	660 ± 76	719 ± 83
215354_s_at PELP1	proline and glutamic acid rich nuclear protein	0.0040	-0.0933	0.1953	-0.1487	0.2547	296 ± 43	314 ± 47	413 ± 43	400 ± 69
214889_x_at PEPP2	phosphoinositide 3-phosphate-binding protein-2	0.0188	-0.0869	0.3103	-0.1503	0.3509	965 ± 95	945 ± 109	1228 ± 203	1265 ± 200
202861_at PER1	period homolog 1	0.0000	-0.0099	0.2052	-0.0479	0.0365	271 ± 55	393 ± 44	479 ± 50	542 ± 107
205251_at PER2	period homolog 2	0.0146	-0.0004	0.1440	-0.2737	0.0063	782 ± 65	883 ± 79	991 ± 63	1156 ± 71
213296_at PEX10	peroxisome biogenesis factor 10	0.2588	-0.0364	-0.1705	0.1926	0.0961	554 ± 44	576 ± 58	568 ± 32	708 ± 32
202464_s_at PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	0.2420	-0.0098	-0.2468	-0.2187	0.0817	1897 ± 261	1863 ± 98	2821 ± 385	2722 ± 458
205261_at PGC	progastresin	0.1265	-0.0029	-0.0870	0.3083	0.0083	164 ± 6	155 ± 16	170 ± 16	291 ± 53
203501_at PGCP	plasma glutamate carboxypeptidase	0.4277	-0.0302	-0.1570	-0.0239	0.2750	430 ± 57	513 ± 66	603 ± 76	556 ± 64
218387_s_at PGLS	6-phosphogluconolactonase	0.0128	-0.0074	0.0406	0.2988	0.0540	719 ± 96	803 ± 82	880 ± 93	1140 ± 147
203314_at PGPL	Pseudoautosomal GTP-binding protein-like	0.0237	-0.0422	-0.2159	-0.2081	0.1991	517 ± 48	492 ± 45	529 ± 36	652 ± 80
220558_x_at PHEMX	pan-hematopoietic expression	0.6180	-0.0087	0.4042	-0.2646	0.0577	393 ± 35	369 ± 25	395 ± 46	572 ± 87
40446_at PHF1	PHD finger protein 1	0.0197	-0.0527	-0.4096	-0.4306	0.0503	2651 ± 90	2777 ± 260	2681 ± 127	3481 ± 378
209439_s_at PHKA2	phosphorylase kinase, α 2	0.0023	-0.0017	-0.0864	-0.3197	0.0079	306 ± 37	299 ± 17	408 ± 35	478 ± 55
218634_at PHLDA3	pleckstrin homology-like domain, family A, member 3	0.0057	-0.0113	0.4370	0.2769	0.0290	709 ± 56	715 ± 78	804 ± 77	1052 ± 124
209345_s_at PI4KII	phosphatidylinositol 4-kinase type II	0.0394	-0.1836	0.0255	-0.1561	0.4015	784 ± 53	835 ± 60	828 ± 52	913 ± 46
212881_at PIAS1	protein inhibitor of activated STAT protein PIAS1	0.0076	-0.0162	0.1215	0.3572	0.0559	334 ± 30	417 ± 89	425 ± 42	598 ± 96
219239_at PIBF1	progesterone-induced blocking factor 1	0.1800	-0.0210	0.3313	-0.0049	0.0412	126 ± 6	140 ± 13	132 ± 14	192 ± 29
200704_at PIG7	LPS-induced TNF-α factor	0.4490	-0.0187	0.4384	-0.3985	0.1091	998 ± 126	909 ± 107	1141 ± 164	1394 ± 49
205281_s_at PIGA	phosphatidylinositol glycan, class A	0.4475	-0.0485	-0.3049	-0.4006	0.3726	276 ± 26	275 ± 19	332 ± 30	320 ± 35
204484_at PIK3C2B	phosphoinositide-3-kinase, class 2, β polypeptide	0.0152	-0.0073	-0.0821	0.1709	0.0169	778 ± 57	744 ± 122	978 ± 107	1382 ± 241
204297_at PIK3C3	phosphoinositide-3-kinase, class 3	0.0844	-0.0010	0.1369	-0.4447	0.0123	321 ± 17	365 ± 31	362 ± 35	487 ± 35
206138_s_at PIK4CB	phosphatidylinositol 4-kinase, catalytic, β polypeptide	0.0327	-0.0035	-0.1265	-0.0494	0.1078	1331 ± 78	1291 ± 88	1500 ± 89	1585 ± 101
222218_s_at PILR	paired immunoglobulin-like receptor α	0.1095	-0.0303	0.2959	-0.2963	0.1310	148 ± 21	181 ± 22	170 ± 17	214 ± 13
209193_at PIM1	pim-1 oncogene	0.1210	-0.0054	-0.0846	-0.4711	0.0680	416 ± 66	362 ± 36	476 ± 62	594 ± 55
214225_at PIN4	protein NIMA-interacting, 4	0.0466	-0.0141	-0.3622	-0.1424	0.0163	180 ± 21	193 ± 16	192 ± 6	276 ± 34
207391_s_at PIP5K1A	phosphatidylinositol 4-phosphate 5-kinase, type I, α	0.0121	-0.0010	0.1322	0.4337	0.0020	724 ± 49	817 ± 53	821 ± 95	1264 ± 143
205570_at PIP5K2A	phosphatidylinositol 4-phosphate 5-kinase, type II, α	0.0308	-0.0089	-0.1953	-0.1431	0.1561	232 ± 26	234 ± 54	276 ± 24	346 ± 49
204145_at PIR51	RAO51-interacting protein	0.0702	-0.0492	0.4145	0.3550	0.1439	65 ± 6	55 ± 6	86 ± 14	104 ± 26
214682_at PKD1	polycystic kidney disease 1	0.0106	-0.3156	-0.0832	0.4934	0.6342	166 ± 28	162 ± 33	212 ± 68	243 ± 62
38269_at PKD2	protein kinase D2	0.0088	-0.0229	0.4274	0.2416	0.0702	603 ± 52	662 ± 96	667 ± 62	868 ± 72
206178_at PLA2G5	phospholipase A2, group V	0.0199	-0.0741	-0.2008	0.1190	0.2547	539 ± 61	498 ± 81	590 ± 98	781 ± 157
215838_s_at PLA2G6	phospholipase A2, group VI	0.0013	-0.0435	0.0710	-0.0647	0.1377	288 ± 23	341 ± 25	381 ± 31	476 ± 114
211918_x_at PLAC3	placenta-specific 3	0.0228	-0.0063	0.0664	-0.1455	0.0137	361 ± 30	428 ± 23	469 ± 50	644 ± 102
205372_at PLAG1	pleiomorphic adenoma gene 1	0.0731	-0.0015	0.0333	0.2767	0.0049	132 ± 13	121 ± 7	168 ± 20	209 ± 19
207943_x_at PLAGL1	pleiomorphic adenoma gene-like 1	0.0851	-0.0128	-0.0981	0.4084	0.0156	275 ± 24	230 ± 25	310 ± 21	334 ± 9
202925_s_at PLAGL2	pleiomorphic adenoma gene-like 2	0.0075	-0.0098	0.4766	-0.2048	0.0607	311 ± 25	327 ± 24	394 ± 15	405 ± 44

Web Table 5 (26)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
205111_s_at PLCE1	phospholipase C, epsilon 1	0.0043	-0.0439	0.1239	-0.3028	0.0336	226 ± 20	286 ± 38	363 ± 46	343 ± 33
204613_at PLCG2	phospholipase C, gamma 2	0.1598	-0.0270	0.3807	0.4970	0.0522	305 ± 30	344 ± 58	301 ± 43	497 ± 77
205034_at PCLL1	phospholipase C-like 1	0.5862	-0.0210	-0.4694	-0.4231	0.2556	405 ± 48	419 ± 75	469 ± 91	594 ± 64
208643_s_at PLD2	phospholipase D2	0.0072	-0.0018	0.0324	-0.0437	0.0098	332 ± 26	417 ± 33	506 ± 40	540 ± 73
201373_at PLEC1	plectin 1, intermediate filament binding protein 500kDa	0.0168	-0.0225	-0.0787	-0.4002	0.1725	406 ± 48	421 ± 17	522 ± 46	606 ± 123
205871_at PLGL	plasminogen-like	0.0840	-0.0107	-0.0372	0.4935	0.0619	151 ± 26	114 ± 20	192 ± 26	217 ± 28
200827_at PLOD	procollagen-lysine, 2-oxoglutarate 5-dioxygenase	0.0550	-0.0284	-0.0271	0.2514	0.1692	409 ± 45	344 ± 12	422 ± 28	517 ± 89
200827_s_at PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0.2114	-0.0263	-0.3160	-0.0328	0.2518	251 ± 29	269 ± 40	267 ± 23	341 ± 39
202185_at PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0.0173	-0.0080	-0.4297	0.4495	0.0720	1010 ± 117	1177 ± 152	1203 ± 94	1520 ± 52
56187_at PLSCR3	phospholipid scramblase 3	0.1117	-0.0403	0.2329	0.2967	0.0088	1539 ± 107	1647 ± 196	1389 ± 51	2309 ± 302
208890_s_at PLXNB2	plexin B2	0.0023	-0.0039	0.0016	-0.1719	0.0193	557 ± 42	905 ± 169	1134 ± 148	1277 ± 242
211014_s_at PML	promyelocytic leukemia	0.1579	-0.0006	0.0435	-0.0359	0.0090	323 ± 19	352 ± 20	353 ± 15	446 ± 38
205991_s_at PMX1	paired mesoderm homeo box 1	0.0076	-0.0227	0.2348	-0.4575	0.0173	178 ± 19	227 ± 28	202 ± 15	285 ± 27
215281_x_at POGZ	pogo transposable element with ZNF domain	0.0119	-0.0094	-0.4953	-0.2406	0.0773	217 ± 30	210 ± 41	314 ± 47	326 ± 35
219380_x_at POLH	polymerase, eta	0.0059	-0.0235	0.0199	-0.0327	0.1005	40 ± 8	51 ± 11	70 ± 17	89 ± 20
209302_at POLR2H	polymerase II polypeptide H	0.0180	-0.0630	0.3990	0.3664	0.2676	965 ± 56	957 ± 91	1036 ± 63	1147 ± 86
203782_s_at POLRMT	polymerase mitochondrial	0.1055	-0.0335	0.3889	0.0304	0.0296	864 ± 15	797 ± 25	837 ± 50	1000 ± 69
210910_s_at POMZP3	POM and ZP3 fusion	0.0001	-0.0058	0.2722	0.1599	0.0309	317 ± 38	321 ± 41	386 ± 53	512 ± 59
204839_at POP5	RNase MRP/RNase P protein-like	0.0807	-0.0192	0.1514	0.4699	0.1272	767 ± 52	800 ± 69	884 ± 56	975 ± 75
207725_at POU4F2	POU domain, class 4, transcription factor 2	0.2444	-0.0179	0.2280	-0.3741	0.0090	85 ± 11	117 ± 15	99 ± 4	156 ± 23
217730_at PP1201	PP1201 protein	0.0066	-0.0546	0.0628	-0.4309	0.0612	481 ± 42	538 ± 103	747 ± 102	696 ± 51
203497_at PP2ABP	PPAR binding protein	0.0989	-0.0008	0.0130	-0.0248	0.0219	219 ± 16	274 ± 16	287 ± 24	323 ± 33
37152_at PPARD	peroxisome proliferative activated receptor, delta	0.0126	-0.0412	0.1345	-0.3681	0.1062	1530 ± 160	1795 ± 206	1959 ± 137	2077 ± 143
202065_s_at PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide	0.0011	-0.0365	0.4079	-0.3017	0.1226	155 ± 14	151 ± 8	197 ± 9	246 ± 59
212841_s_at PPFIBP2	PTPRF interacting protein, binding protein 2	0.0484	-0.1761	-0.2569	-0.4983	0.8289	392 ± 66	386 ± 64	454 ± 68	492 ± 57
208993_s_at PPIG	peptidyl-prolyl isomerase G	0.0083	-0.5287	0.0029	-0.0878	0.3766	518 ± 51	638 ± 50	650 ± 52	628 ± 92
220158_at PPL13	placental protein 13-like protein	0.3020	-0.0314	0.4667	-0.3886	0.1124	208 ± 22	208 ± 15	208 ± 16	281 ± 38
209296_at PPM1B	protein phosphatase 1B, magnesium-dependent, beta isoform	0.1784	-0.0386	-0.0717	-0.3369	0.4205	1708 ± 174	1626 ± 213	1967 ± 249	2108 ± 254
204566_at PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	0.3476	-0.0262	-0.2363	-0.4974	0.1160	263 ± 22	267 ± 31	251 ± 30	350 ± 36
200726_at PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	0.1435	-0.0081	-0.1204	-0.2027	0.1911	2398 ± 123	2317 ± 420	2673 ± 189	3037 ± 202
212680_x_at PPP1R14B	protein phosphatase 1, regulatory subunit 14B	0.1825	-0.0314	0.4801	0.3522	0.0832	276 ± 33	226 ± 49	285 ± 40	438 ± 93
202014_at PPP1R15A	protein phosphatase 1, regulatory subunit 15A	0.0098	-0.0082	0.3147	0.0340	0.0366	186 ± 36	146 ± 20	211 ± 21	394 ± 109
205478_at PPP1R1A	protein phosphatase 1, regulatory subunit 1A	0.6284	-0.0239	-0.3431	-0.1275	0.1149	545 ± 34	533 ± 41	720 ± 33	848 ± 199
221088_s_at PPP1R9A	protein phosphatase 1, regulatory subunit 9A	0.0211	-0.2320	0.3029	-0.3311	0.3112	447 ± 53	382 ± 27	519 ± 61	582 ± 120
202883_s_at PPP2R1B	protein phosphatase 2, regulatory subunit A, beta isoform	0.0391	-0.0201	-0.1117	-0.1160	0.2970	653 ± 51	691 ± 63	745 ± 27	808 ± 90
216105_x_at PPP2R4	protein phosphatase 2A, regulatory subunit B'	0.0346	-0.9433	-0.2356	0.4966	0.3095	794 ± 38	739 ± 55	931 ± 85	769 ± 112
211159_s_at PPP2R5D	protein phosphatase 2, regulatory subunit B, delta isoform	0.0359	-0.2226	-0.0117	0.2715	0.3967	196 ± 19	195 ± 17	208 ± 2	233 ± 21
209826_at PPT2	palmitoyl-protein thioesterase 2	0.0048	-0.5098	0.1746	0.1236	0.7143	296 ± 20	304 ± 85	302 ± 46	380 ± 73
204086_at PRAME	preferentially expressed antigen in melanoma	0.5153	-0.0447	0.1751	-0.2056	0.3703	173 ± 30	156 ± 16	175 ± 22	231 ± 41
201494_at PRCP	prolylcarboxypeptidase	0.5735	-0.0345	-0.4344	-0.0348	0.4317	1333 ± 123	1500 ± 109	1544 ± 168	1687 ± 201
203057_s_at PRDM2	PR domain containing 2, with ZNF domain	0.0299	-0.0576	0.4258	-0.1576	0.0737	376 ± 28	513 ± 62	444 ± 40	558 ± 73
37022_at PRELP	proline arginine-rich end leucine-rich repeat protein	0.1874	-0.0079	0.0762	-0.3172	0.0407	698 ± 48	859 ± 86	837 ± 53	1062 ± 142

Web Table 5 (27)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
204842_x_at PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, α	0.0028	-0.0302	0.0249	-0.2060	0.0425	709 \pm 64	984 \pm 147	935 \pm 68	1283 \pm 234
204745_s_at PRKCABP	protein kinase C, α binding protein	0.0474	-0.0758	0.1434	-0.2528	0.1499	391 \pm 31	458 \pm 71	446 \pm 29	561 \pm 72
202161_at PRKCL1	protein kinase C-like 1	0.0084	-0.0231	0.0854	0.4515	0.1113	310 \pm 14	361 \pm 26	438 \pm 38	515 \pm 74
204211_x_at PRKR	protein kinase, interferon-inducible d.s.RNA dependent	0.0103	-0.0043	0.0395	-0.0064	0.0251	246 \pm 21	330 \pm 33	325 \pm 28	450 \pm 78
39313_at PRKWNK1	protein kinase, lysine deficient 1	0.0064	-0.0496	0.0526	-0.3309	0.1312	152 \pm 17	208 \pm 36	229 \pm 35	286 \pm 48
204061_at PRKX	protein kinase, X-linked	0.1732	-0.0020	-0.0415	0.2905	0.0240	294 \pm 40	215 \pm 21	345 \pm 35	435 \pm 73
205445_at PRL	prolactin	0.4842	-0.0011	0.0380	-0.0237	0.0194	170 \pm 7	198 \pm 24	179 \pm 5	252 \pm 29
216638_s_at PRLR	prolactin receptor	0.4675	-0.0855	-0.1510	0.4310	0.0176	57 \pm 12	50 \pm 9	38 \pm 10	104 \pm 22
220696_at PRO478	PRO478 protein	0.1663	-0.0464	0.0283	-0.0020	0.0355	69 \pm 12	90 \pm 12	136 \pm 21	92 \pm 18
207401_at PROX1	prospero-related homeobox 1	0.0419	-0.0341	0.0247	0.2964	0.0547	68 \pm 14	51 \pm 11	80 \pm 12	105 \pm 13
202126_at PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B	0.0258	-0.0201	0.0247	-0.2297	0.0927	1002 \pm 53	1076 \pm 41	1159 \pm 63	1199 \pm 72
200000_s_at PRPF8	PRP8 pre-mRNA processing factor 8 homolog	0.0081	-0.0126	-0.2210	0.4400	0.0224	1501 \pm 72	1369 \pm 71	1551 \pm 80	1732 \pm 41
208017_s_at PRSS15	protease, serine, 15	0.0418	-0.0462	0.3570	0.1826	0.1744	759 \pm 43	781 \pm 98	783 \pm 78	1053 \pm 75
202880_s_at PSCD1	pleckstrin homology, Sec7 and coiled/coil domains 1	0.0186	-0.0142	0.0530	-0.0749	0.0937	531 \pm 31	730 \pm 103	799 \pm 98	899 \pm 70
203399_x_at PSG3	pregnancy specific β -1-glycoprotein 3	0.2826	-0.0111	0.1048	-0.1009	0.2034	71 \pm 9	82 \pm 13	76 \pm 15	111 \pm 18
201053_s_at PSMF1	proteasome inhibitor subunit 1	0.5086	-0.0246	0.1422	-0.0754	0.1961	443 \pm 38	514 \pm 50	499 \pm 31	586 \pm 63
215233_at PSR	phosphatidylserine receptor	0.0030	-0.1146	-0.0022	0.3050	0.0887	237 \pm 31	113 \pm 31	363 \pm 75	327 \pm 103
216306_x_at PTBP1	polypyrimidine tract binding protein 1	0.0000	-0.0080	-0.3438	-0.1018	0.0139	555 \pm 76	763 \pm 67	1021 \pm 101	962 \pm 90
209815_at PTCH	patched homolog	0.3840	-0.0278	-0.3552	-0.1513	0.1068	580 \pm 57	556 \pm 45	760 \pm 94	713 \pm 35
211252_x_at PTCRA	pre-T-cell receptor α precursor	0.0739	-0.0054	0.0513	-0.1717	0.0429	436 \pm 31	557 \pm 77	578 \pm 60	713 \pm 93
221005_s_at PTDS2	phosphatidylserine synthase 2	0.0767	-0.0374	0.2876	-0.2261	0.1245	300 \pm 26	301 \pm 15	404 \pm 46	383 \pm 50
210702_s_at PTGIS	prostaglandin I ₂ synthase	0.0487	-0.0404	0.0043	-0.1266	0.0582	54 \pm 9	94 \pm 13	88 \pm 20	126 \pm 27
205128_x_at PTGS1	prostaglandin-endoperoxide synthase 1	0.0239	-0.0967	0.0116	-0.1446	0.1213	386 \pm 39	521 \pm 47	500 \pm 62	571 \pm 62
205911_at PTHR1	parathyroid hormone receptor 1	0.0004	-0.0490	0.0360	-0.4442	0.0721	329 \pm 20	454 \pm 74	514 \pm 48	551 \pm 100
211921_x_at PTMA	prothymosin, α	0.0417	-0.0372	0.2769	-0.2721	0.2916	3270 \pm 222	3812 \pm 583	4248 \pm 432	4259 \pm 440
208617_s_at PTP4A2	protein tyrosine phosphatase type IVA, member 2	0.1686	-0.0346	0.4635	-0.2168	0.2035	4403 \pm 445	4600 \pm 465	5632 \pm 441	5320 \pm 491
209695_at PTP4A3	protein tyrosine phosphatase type IVA, member 3	0.0443	-0.2697	0.4945	0.4491	0.5277	419 \pm 38	394 \pm 20	508 \pm 46	492 \pm 111
200635_s_at PTPRF	protein tyrosine phosphatase, receptor type, F	0.0131	-0.2112	0.4725	-0.0859	0.1438	329 \pm 29	369 \pm 28	469 \pm 21	398 \pm 76
208300_at PTPRH	protein tyrosine phosphatase, receptor type, H	0.0395	-0.1087	0.4328	-0.3639	0.1764	141 \pm 18	163 \pm 14	164 \pm 20	219 \pm 39
203038_at PTPRK	protein tyrosine phosphatase, receptor type, K	0.0062	-0.0039	-0.1297	-0.2852	0.0461	1992 \pm 286	2153 \pm 376	2732 \pm 224	3066 \pm 245
208789_at PTRF	polymerase I and transcript release factor	0.0011	-0.0027	0.2795	-0.1749	0.0513	604 \pm 87	709 \pm 124	1004 \pm 125	1088 \pm 209
200677_at PTTG1IP	pituitary tumor-transforming 1 interacting protein	0.0351	-0.0001	-0.2915	-0.2062	0.0046	2393 \pm 185	2503 \pm 330	3374 \pm 265	3682 \pm 326
201164_s_at PUM1	pumilio homolog 1	0.0068	0.6643	-0.4315	0.0272	0.5530	968 \pm 50	865 \pm 38	1012 \pm 88	895 \pm 118
204021_s_at PURA	purine-rich element binding protein A	0.0964	-0.0050	-0.0979	0.1572	0.0017	776 \pm 70	603 \pm 36	770 \pm 54	1200 \pm 161
201087_at PXN	paxillin	0.0233	-0.0361	0.1051	-0.0319	0.2670	602 \pm 53	649 \pm 37	735 \pm 81	780 \pm 89
207330_at PZP	pregnancy-zone protein	0.1449	-0.0106	0.0668	-0.4680	0.0022	227 \pm 28	328 \pm 55	229 \pm 18	448 \pm 56
217846_at QARS	glutaminyl-tRNA synthetase	0.0059	-0.0209	0.0045	-0.1218	0.0880	1227 \pm 65	1356 \pm 76	1427 \pm 89	1581 \pm 148
212636_at QKI	homolog of mouse quaking QKI	0.0005	-0.0010	0.0054	-0.0078	0.0031	6635 \pm 488	9010 \pm 882	1099 \pm 793	9882 \pm 1262
210714_at R3HDM	R3H domain containing	0.0035	-0.0503	-0.4702	0.4698	0.1971	219 \pm 31	216 \pm 45	268 \pm 52	374 \pm 90
217793_at RAB11B	RAB11B, member RAS oncogene family	0.0501	-0.0496	0.1744	-0.1866	0.2098	336 \pm 36	297 \pm 35	348 \pm 29	484 \pm 112
202252_at RAB13	RAB13, member RAS oncogene family	0.0001	-0.0049	0.2138	-0.3645	0.0056	897 \pm 127	1125 \pm 163	1695 \pm 171	1586 \pm 223
220964_s_at RAB1B	RAB1B, member RAS oncogene family	0.0197	-0.5264	0.0471	-0.0233	0.3043	814 \pm 93	1064 \pm 130	1187 \pm 103	1010 \pm 241

Web Table 5 (28)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
208730_x_at	RAB2, member RAS oncogene family	0.0716	-0.0388	0.0827	-0.0213	0.0418	511 ± 45	627 ± 41	578 ± 78	870 ± 153
218360_at	RAB22A, member RAS oncogene family	0.1373	-0.0065	0.2237	-0.1059	0.0137	289 ± 21	337 ± 19	306 ± 24	389 ± 17
217763_s_at	RAB31, member RAS oncogene family	0.0208	-0.0035	0.1143	-0.3723	0.0129	1585 ± 103	1671 ± 198	2164 ± 133	2199 ± 186
213531_s_at	RAB3 GTPase-ACTIVATING PROTEIN	0.0411	-0.2783	-0.3024	0.4026	0.4796	3895 ± 362	3823 ± 552	4573 ± 696	5071 ± 894
203223_at	rabaptin-5	0.0111	-0.0026	0.1192	-0.0265	0.0280	64 ± 10	100 ± 14	97 ± 16	137 ± 22
208641_s_at	ras-related C3 botulinum toxin substrate 1	0.0418	-0.1343	0.4572	0.1130	0.1295	5866 ± 525	5738 ± 741	5720 ± 521	7954 ± 1103
204461_x_at	RAD1 homolog	0.0219	-0.1051	0.0180	0.2628	0.1006	349 ± 32	361 ± 58	481 ± 44	502 ± 72
221523_s_at	Rag D protein	0.0095	-0.0593	0.1697	0.0922	0.2760	619 ± 32	617 ± 51	654 ± 42	748 ± 79
218849_s_at	RelA-associated inhibitor	0.0013	-0.0004	0.0638	-0.0486	0.0016	328 ± 32	451 ± 31	451 ± 43	703 ± 108
212124_at	retinoic acid induced 17	0.6879	-0.0375	-0.0374	-0.2345	0.1936	1912 ± 97	1941 ± 116	2173 ± 54	2087 ± 113
214435_x_at	v-rat simian leukemia viral oncogene homolog A	0.0239	-0.0250	0.0850	0.4558	0.0393	251 ± 13	274 ± 28	274 ± 14	369 ± 52
202844_s_at	ralA binding protein 1	0.2793	-0.0415	-0.3200	-0.4585	0.0736	485 ± 54	438 ± 38	459 ± 19	606 ± 54
209050_s_at	ral guanine nucleotide dissociation stimulator	0.0006	-0.0052	-0.4854	0.4162	0.0197	2780 ± 314	2596 ± 203	3981 ± 659	6540 ± 1705
210552_s_at	Ral guanine nucleotide exchange factor RalGPS1A	0.3669	-0.0258	0.0968	-0.2394	0.3475	110 ± 8	121 ± 12	123 ± 13	148 ± 23
210271_s_at	RALY	0.2539	-0.0393	0.3665	0.2195	0.1213	490 ± 59	382 ± 36	477 ± 51	612 ± 80
204916_at	receptor activity modifying protein 1	0.1731	-0.0038	0.0603	0.4486	0.0316	866 ± 64	841 ± 51	962 ± 56	1099 ± 71
202640_s_at	RAN binding protein 3	0.0251	-0.0191	-0.3513	-0.3009	0.0114	381 ± 26	350 ± 34	543 ± 52	485 ± 56
212127_at	Ran GTPase activating protein 1	0.0015	-0.2068	-0.2733	-0.4353	0.3901	551 ± 64	582 ± 35	607 ± 72	766 ± 163
209285_s_at	KIAA1105 protein	0.0654	-0.0039	0.1381	-0.0103	0.0547	918 ± 67	1160 ± 142	1252 ± 71	1279 ± 119
205080_at	retinoic acid receptor, β	0.1443	-0.0395	-0.1468	0.4361	0.0861	341 ± 42	322 ± 31	345 ± 18	451 ± 44
209496_at	retinoic acid receptor responder 2	0.0109	-0.0005	0.3095	0.2327	0.0043	281 ± 38	319 ± 47	414 ± 38	529 ± 64
204070_at	retinoic acid receptor responder 3	0.0720	-0.0326	0.3585	-0.1098	0.2308	498 ± 48	522 ± 77	633 ± 52	619 ± 36
214368_at	RAS guanyl releasing protein 2	0.0269	-0.2404	-0.3323	-0.3678	0.0837	43 ± 11	71 ± 21	113 ± 18	85 ± 24
219214_s_at	RB-associated KRAB repressor	0.0374	-0.3075	0.0094	-0.4507	0.1300	117 ± 10	188 ± 18	149 ± 27	181 ± 34
205062_x_at	retinoblastoma binding protein 1	0.0209	-0.2634	0.0245	0.3884	0.3650	223 ± 15	230 ± 18	260 ± 16	258 ± 24
202040_s_at	retinoblastoma binding protein 2	0.0024	-0.0106	0.1014	-0.3293	0.0346	535 ± 53	598 ± 73	644 ± 27	811 ± 96
205169_at	retinoblastoma binding protein 5	0.0463	-0.3678	-0.3349	-0.0385	0.7640	165 ± 13	176 ± 18	179 ± 25	196 ± 27
212781_at	retinoblastoma binding protein 6	0.0095	-0.2117	0.0381	-0.3574	0.2409	398 ± 32	464 ± 60	506 ± 27	476 ± 38
205236_at	retinoblastoma-like 1	0.0004	-0.0027	0.0106	-0.0012	0.0095	41 ± 6	77 ± 11	99 ± 10	109 ± 25
209884_x_at	RNA binding motif protein 10	0.0000	-0.0610	0.0963	-0.4212	0.0690	396 ± 27	448 ± 43	627 ± 55	611 ± 130
219286_s_at	RNA binding motif protein 15	0.0074	-0.0401	-0.0558	0.4091	0.0318	602 ± 62	457 ± 33	856 ± 127	787 ± 110
222026_at	RNA binding motif protein 3	0.0245	-0.3758	0.1587	0.3906	0.6027	263 ± 23	274 ± 27	321 ± 23	310 ± 65
219867_at	RNA binding motif protein 6	0.0196	-0.0963	0.1343	-0.2604	0.2455	1276 ± 201	1245 ± 126	1734 ± 212	1591 ± 230
213852_at	RNA binding motif, single stranded interacting protein 8A	-0.9563	-0.0198	0.0006	-0.1022	0.0384	1490 ± 72	1804 ± 46	1806 ± 80	1888 ± 173
215127_s_at	RNA binding motif, single stranded interacting protein 1	0.1620	-0.0343	0.2688	-0.1520	0.2489	606 ± 45	595 ± 64	745 ± 70	740 ± 94
34187_at	RNA binding motif, single stranded interacting protein 2	0.0003	-0.0097	0.2625	-0.0838	0.0413	61 ± 10	61 ± 7	95 ± 10	101 ± 18
206767_at	RNA binding motif, single stranded interacting protein	0.1478	-0.0101	0.1234	-0.3970	0.0487	340 ± 33	353 ± 35	427 ± 23	459 ± 41
209487_at	RNA-binding protein gene with multiple splicing	0.0071	-0.0116	0.1152	0.2701	0.0534	284 ± 25	245 ± 53	366 ± 67	386 ± 55
219382_at	RPA-binding trans-activator	0.0045	-0.0001	0.2426	-0.0062	0.0014	207 ± 24	334 ± 12	346 ± 20	478 ± 55
212977_at	G protein-coupled receptor	0.0326	-0.0115	-0.3993	-0.0569	0.0410	233 ± 21	274 ± 39	359 ± 40	348 ± 41
219155_at	retinal degeneration B β	0.0027	-0.0079	0.2426	0.4367	0.0486	635 ± 58	702 ± 107	881 ± 78	929 ± 92
219799_s_at	NADP-dependent retinol dehydrogenase/reductase	0.4356	-0.0359	0.0517	-0.1756	0.0119	294 ± 32	447 ± 68	336 ± 44	534 ± 59

Web Table 5 (29)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
218599_at REC8	Rec8p, cohesion phosphoprotein of the rad21p family	0.2758	-0.0067	-0.2864	-0.1630	0.0510	367 ± 26	411 ± 53	409 ± 28	513 ± 33
211168_s_at RENT1	regulator of nonsense transcripts 1	0.0101	-0.0006	0.3164	0.3478	0.0013	463 ± 22	468 ± 33	507 ± 30	676 ± 58
203600_s_at RES4-22	gene with multiple splice variants near HD locus on 4p16.3	0.0236	-0.0741	0.3668	0.2766	0.1669	867 ± 26	965 ± 60	939 ± 72	1072 ± 80
214661_s_at RES4-25	homology to hypothetical S. pombe gene	0.0988	-0.0121	0.3328	0.3937	0.0102	265 ± 13	290 ± 29	271 ± 11	383 ± 40
212920_at REST	RE1-silencing transcription factor	0.0366	-0.0166	-0.2577	0.4119	0.0974	145 ± 11	141 ± 13	162 ± 21	194 ± 14
212968_at RFNG	radical fringe homolog	0.0014	-0.1213	-0.3207	0.3628	0.1974	424 ± 13	410 ± 22	484 ± 16	516 ± 18
207672_at RFX4	regulatory factor X, 4	0.2115	-0.0018	-0.3907	-0.4004	0.0403	64 ± 18	87 ± 14	143 ± 34	184 ± 48
210751_s_at RGN	regucalcin	0.0604	-0.0079	0.1159	-0.1632	0.0119	399 ± 36	473 ± 48	486 ± 19	610 ± 55
209639_s_at RGS12	regulator of G-protein signalling 12	0.0082	-0.0547	0.4138	-0.4777	0.1434	175 ± 15	177 ± 20	230 ± 30	259 ± 44
209324_s_at RGS16	regulator of G-protein signalling 16	0.1043	-0.0036	-0.2729	-0.4144	0.0083	328 ± 30	341 ± 34	366 ± 43	517 ± 46
207525_s_at RGS19IP1	regulator of G-protein signalling 19 interacting protein 1	0.0238	-0.1713	0.0105	-0.4184	0.2236	885 ± 24	1039 ± 77	1068 ± 64	1157 ± 63
206518_s_at RGS9	regulator of G-protein signalling 9	0.0317	-0.2786	0.0287	-0.4574	0.5473	88 ± 6	110 ± 11	107 ± 23	120 ± 11
213409_s_at RHEB2	Ras homolog enriched in brain 2	0.0509	-0.0136	0.1401	-0.0536	0.0964	148 ± 18	172 ± 23	179 ± 14	211 ± 6
202975_s_at RHOBTB3	Rho-related BTB domain containing 3	0.0003	-0.0403	0.1039	-0.2136	0.0129	1350 ± 103	1632 ± 149	2138 ± 216	1942 ± 184
203596_s_at RI58	retinoid acid- and interferon-inducible protein	0.1430	-0.0348	-0.0773	0.3114	0.0765	353 ± 14	284 ± 54	382 ± 11	416 ± 33
218076_s_at RICH1	homolog of rat nadrin	0.0152	-0.0003	0.2587	-0.0162	0.0030	536 ± 39	621 ± 47	614 ± 49	883 ± 99
221126_at RIG	regulated in glioma	0.0037	-0.0549	0.4428	-0.2707	0.1835	79 ± 10	82 ± 11	104 ± 14	132 ± 32
211564_s_at RIL	LM domain protein	0.1519	-0.0077	0.2047	0.4985	0.0250	118 ± 16	177 ± 24	172 ± 27	256 ± 45
60471_at RIN3	Ras and Rab interactor 3	0.0120	-0.0003	0.1182	-0.2578	0.0065	302 ± 40	345 ± 41	402 ± 55	654 ± 121
219312_s_at RINZF	zinc finger protein RINZF	0.0077	-0.0001	0.0259	-0.0048	0.0024	53 ± 4	64 ± 9	87 ± 9	92 ± 5
219041_s_at RIP60	replication initiation region protein	0.0112	-0.0015	0.2236	0.3474	0.0019	986 ± 67	921 ± 60	1290 ± 99	1351 ± 78
211753_s_at RLN1	relaxin 1	0.0437	-0.0016	0.2236	0.1966	0.0036	79 ± 9	85 ± 18	90 ± 8	154 ± 20
210524_x_at RNAHP	RNA helicase-related protein	0.4991	-0.0261	0.3426	-0.0369	0.0738	3327 ± 296	4122 ± 268	3837 ± 200	5610 ± 1181
213397_x_at RNASE4	ribonuclease, RNase A family, 4	0.0777	-0.0118	-0.2765	-0.3788	0.1338	279 ± 31	307 ± 26	303 ± 23	397 ± 56
217984_at RNASE6PL	ribonuclease 6 precursor	0.7632	-0.0432	0.0616	-0.0270	0.0356	1671 ± 133	2260 ± 119	1887 ± 199	2454 ± 283
203022_at RNASEH2A	ribonuclease H2, large subunit	0.0821	-0.0344	0.0285	-0.3617	0.0019	262 ± 18	311 ± 37	247 ± 7	380 ± 13
221154_at RNF18	ring finger protein 18	0.0296	-0.0216	-0.1136	-0.4719	0.0072	37 ± 9	36 ± 4	31 ± 6	79 ± 16
210706_s_at RNF24	ring finger protein 24	0.4464	-0.0308	0.1965	-0.2842	0.2294	535 ± 33	497 ± 51	554 ± 29	634 ± 65
203160_s_at RNF8	ring finger protein 8	0.0158	-0.2849	-0.2667	0.4711	0.3334	487 ± 18	444 ± 24	453 ± 31	526 ± 54
211387_x_at RNGTT	RNA guanylyltransferase and 5'-phosphatase	0.1952	-0.0283	0.0856	-0.0485	0.2043	235 ± 25	249 ± 32	336 ± 40	338 ± 69
212430_at RNPC1	RNA-binding region containing 1	0.0016	-0.0538	0.2544	-0.2201	0.1628	324 ± 39	390 ± 42	446 ± 29	478 ± 86
218301_at RNPEPL1	arginyl aminopeptidase-like 1	0.0413	-0.0314	-0.4549	-0.2899	0.1225	241 ± 34	239 ± 32	305 ± 18	348 ± 53
210230_at RNU2	RNA, U2 small nuclear	0.0326	-0.1111	0.0421	-0.3610	0.4191	164 ± 45	273 ± 83	334 ± 95	419 ± 194
213044_at ROCK1	Rho-associated, coiled-coil containing protein kinase 1	0.0912	-0.0066	-0.2032	-0.0507	0.0977	1312 ± 131	1316 ± 87	1642 ± 116	1592 ± 111
214697_s_at ROD1	ROD1 regulator of differentiation 1	0.0344	-0.1326	0.0389	-0.1794	0.4233	63 ± 8	76 ± 12	67 ± 14	92 ± 17
207569_at ROS1	v-ros UR2 sarcoma virus oncogene homolog 1	0.2563	-0.0038	0.1150	0.2559	0.0252	97 ± 8	87 ± 10	115 ± 8	145 ± 22
206169_x_at RoXaN	ubiquitous tetrapeptide containing protein RoXaN	0.0425	-0.0857	0.0190	-0.2736	0.1373	266 ± 33	380 ± 84	450 ± 54	399 ± 60
205191_at RPA40	retinitis pigmentosa 2	0.1129	-0.0490	-0.4458	-0.3696	0.0698	85 ± 13	93 ± 9	131 ± 16	112 ± 10
207515_s_at RPA40	RNA polymerase I subunit	0.0081	-0.0308	0.3626	0.1519	0.0682	322 ± 23	289 ± 12	360 ± 26	437 ± 65
210573_s_at RPC62	polymerase III	0.1680	-0.0280	0.2938	-0.2901	0.0138	225 ± 19	273 ± 35	246 ± 25	377 ± 46
206608_s_at RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	0.1067	-0.0091	0.4838	-0.1302	0.0166	197 ± 25	229 ± 13	193 ± 16	327 ± 55
200725_x_at RPL10	ribosomal protein L10	0.0003	-0.1119	0.3732	-0.4860	0.2923	5597 ± 425	6042 ± 561	6726 ± 452	6950 ± 795

Web Table 5 (30)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
212933_x_at	ribosomal protein L13	0.0008	-0.0258	0.0261	0.3873	0.0595	7513 ± 381	8578 ± 982	9468 ± 458	10087 ± 800
200715_x_at	ribosomal protein L13a	0.0009	-0.0003	0.1337	0.2796	0.0004	2416 ± 99	2801 ± 288	3103 ± 293	4234 ± 331
200022_at	ribosomal protein L18	0.0171	-0.2639	-0.2083	-0.3094	0.5468	4784 ± 300	4818 ± 203	5286 ± 88	5108 ± 407
213642_at	ribosomal protein L27	0.0821	-0.0035	0.0880	-0.1178	0.0125	304 ± 30	377 ± 36	394 ± 14	539 ± 85
212044_s_at	ribosomal protein L27a	0.1105	-0.0133	0.1608	-0.2125	0.0158	336 ± 32	376 ± 44	353 ± 15	517 ± 163
200003_s_at	ribosomal protein L28	0.0400	-0.5973	-0.4237	-0.3188	0.2660	6713 ± 424	6945 ± 420	8190 ± 391	6931 ± 786
214041_x_at	ribosomal protein L37a	0.0023	-0.0101	0.2570	-0.2179	0.0355	700 ± 67	962 ± 216	1143 ± 93	1689 ± 418
208695_s_at	ribosomal protein L39	0.0024	-0.0154	-0.2328	-0.0623	0.0702	12858 ± 725	12490 ± 725	15140 ± 764	14521 ± 936
200089_s_at	ribosomal protein L4	0.0164	-0.2430	0.2975	0.3698	0.0167	5922 ± 227	5918 ± 255	7235 ± 393	6300 ± 786
200909_s_at	ribosomal protein, large P2	0.0314	-0.1173	-0.1384	-0.4765	0.2375	5678 ± 292	5163 ± 197	6380 ± 415	6217 ± 571
220113_x_at	similar to DNA-directed RNA polymerase I	0.0667	-0.0032	0.0672	-0.0129	0.0427	902 ± 66	997 ± 95	1427 ± 189	1444 ± 235
214001_x_at	ribosomal protein S10	0.0045	-0.0073	0.0694	-0.0138	0.0169	227 ± 34	364 ± 52	319 ± 29	477 ± 81
213414_s_at	ribosomal protein S19	0.0216	-0.0189	-0.1150	-0.3807	0.2190	8397 ± 545	7998 ± 597	8966 ± 388	9804 ± 356
208903_at	ribosomal protein S28	0.0054	-0.2684	-0.0993	0.2320	0.3472	652 ± 27	717 ± 84	698 ± 47	793 ± 161
213347_x_at	ribosomal protein S4, X-linked	0.0207	-0.1661	0.1692	0.3259	0.0430	10105 ± 387	11438 ± 817	12669 ± 774	11631 ± 183
203379_at	ribosomal protein S6 kinase, 90kDa, polypeptide 1	0.0073	-0.0290	0.3845	-0.1808	0.0977	346 ± 68	350 ± 38	576 ± 70	583 ± 142
204633_s_at	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.0388	-0.0032	-0.1274	-0.1023	0.0742	854 ± 48	946 ± 105	1126 ± 101	1139 ± 103
201204_s_at	ribosome binding protein 1 homolog 180kDa	0.0020	-0.0366	0.3385	-0.2930	0.0486	611 ± 119	841 ± 164	1277 ± 140	1180 ± 282
203704_s_at	ras responsive element binding protein 1	0.1249	-0.0122	0.2622	-0.1804	0.0544	278 ± 32	315 ± 27	347 ± 10	407 ± 48
209527_at	homolog of Yeast RRP4, 3'-5'-exoribonuclease	0.0298	-0.1503	-0.1453	0.2872	0.1576	334 ± 14	291 ± 14	382 ± 45	390 ± 45
RUZS		0.0018	-0.0404	0.1196	-0.4033	0.0483	729 ± 88	946 ± 135	874 ± 67	1678 ± 486
222368_at	RUN and FYVE domain-containing 1	0.0314	-0.0182	0.3917	0.3117	0.0481	1108 ± 76	1113 ± 130	1163 ± 45	1508 ± 159
218243_at	run-related transcription factor 2	0.0766	-0.0420	0.2358	-0.0082	0.1172	103 ± 15	136 ± 21	122 ± 20	181 ± 34
216994_s_at	retinoid X receptor, β	0.0056	-0.3866	0.0000	-0.2507	0.1774	859 ± 39	981 ± 58	1037 ± 51	975 ± 90
209148_at	retinoid X receptor, γ	0.0168	-0.0065	0.2179	0.4743	0.0058	160 ± 16	194 ± 21	201 ± 10	251 ± 18
205954_at	RING1 and YY1 binding protein	0.0457	-0.0454	0.3750	0.3441	0.0022	1330 ± 164	1487 ± 190	1111 ± 54	2029 ± 142
RYBP	RYK receptor-like tyrosine kinase	0.5209	-0.0458	0.4641	-0.3741	0.3495	178 ± 19	175 ± 17	196 ± 15	222 ± 27
214172_x_at	S100 calcium binding protein A12	0.4581	-0.0009	-0.4202	-0.2978	0.0230	150 ± 28	120 ± 17	166 ± 17	285 ± 64
208663_at	S100 calcium binding protein A14	0.1051	-0.0343	-0.0895	0.3152	0.0153	560 ± 60	506 ± 14	514 ± 49	753 ± 67
208540_x_at	S100 calcium binding protein A4	0.2738	-0.0267	0.4680	-0.0031	0.2427	176 ± 49	270 ± 80	312 ± 62	386 ± 93
203166_s_at	SUMO-1 activating enzyme subunit 1	0.0190	-0.3629	0.0755	-0.4510	0.5748	890 ± 41	909 ± 40	985 ± 56	959 ± 74
217946_s_at	SAE1	0.0072	-0.0010	0.2105	-0.2087	0.0156	122 ± 12	135 ± 18	166 ± 11	201 ± 28
213635_s_at	scaffold attachment factor B	0.0138	-0.0267	0.3549	0.4857	0.0426	1603 ± 122	1758 ± 94	1682 ± 115	2089 ± 136
SALL2	sall-like 2	0.3324	-0.0208	-0.3346	-0.2982	0.1064	446 ± 21	468 ± 67	432 ± 50	625 ± 91
204900_x_at	sin3-associated polypeptide, 30kDa	0.0041	-0.0332	0.3963	0.3809	0.1055	459 ± 33	485 ± 55	578 ± 49	620 ± 69
SAP30	squamous cell carcinoma antigen recognised by T cells	0.6623	-0.0164	-0.0957	-0.1797	0.1772	256 ± 26	244 ± 33	261 ± 26	334 ± 24
SART1	squamous cell carcinoma antigen recognized by T cell	0.1117	-0.0446	0.0468	-0.0322	0.1945	1098 ± 106	1315 ± 150	1433 ± 99	1431 ± 159
SART2	sarcoma amplified sequence	0.0055	-0.0196	0.3385	-0.2880	0.0722	743 ± 65	843 ± 66	856 ± 40	1083 ± 153
SAS	secretory carrier membrane protein 2	0.6291	-0.0126	-0.0764	0.4019	0.0953	899 ± 80	827 ± 42	971 ± 88	1126 ± 80
SCAMP2	secretory carrier membrane protein 3	0.3737	-0.0220	0.0549	-0.1425	0.0429	547 ± 34	559 ± 26	517 ± 37	685 ± 60
SCAMP3	scavenger receptor class B, member 1	0.1838	-0.0444	0.0003	-0.2152	0.0233	108 ± 6	139 ± 12	118 ± 12	151 ± 10
SCARB1	putative selenocysteine lyase	0.0150	-0.0517	0.3018	-0.4003	0.2333	708 ± 71	756 ± 119	828 ± 62	1023 ± 182
SCRIB	scribble									

Web Table 5 (31)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
221513_s_at	SDCCAG16	0.0572	-0.0409	0.1271	-0.4150	0.3428	301 ± 9	281 ± 15	326 ± 19	346 ± 44
218427_at	SDCCAG3	0.0432	-0.0235	-0.1022	-0.2134	0.2393	250 ± 38	239 ± 13	298 ± 41	328 ± 26
212609_s_at	SDCCAG8	0.0423	-0.2550	0.1802	0.4689	0.3989	936 ± 79	979 ± 78	1105 ± 107	1100 ± 38
221621_at	SEC14L1	0.2649	-0.0188	0.0533	-0.0364	0.0882	135 ± 14	141 ± 10	140 ± 11	196 ± 31
204541_at	SEC14L2	0.0028	-0.0011	0.1077	0.2310	0.0006	181 ± 16	184 ± 21	289 ± 23	321 ± 34
218703_at	SEC22A	0.2462	-0.0275	0.1275	0.2372	0.1031	148 ± 16	148 ± 22	151 ± 16	212 ± 28
212900_at	SEC24A	0.2023	-0.0090	0.1276	-0.0804	0.0915	548 ± 47	563 ± 78	647 ± 50	767 ± 83
202361_at	SEC24C	0.0432	-0.0408	-0.0916	0.3909	0.1990	606 ± 33	593 ± 27	693 ± 64	728 ± 67
201914_s_at	SEC63L	0.0650	-0.0238	0.0097	-0.4574	0.0479	230 ± 6	244 ± 25	292 ± 12	322 ± 42
213716_s_at	SECTM1	0.6746	-0.0168	0.2184	-0.4093	0.2470	118 ± 23	102 ± 8	138 ± 38	270 ± 20
204563_at	SELL	0.1906	-0.0181	0.2189	-0.2847	0.0964	250 ± 35	309 ± 45	290 ± 48	424 ± 68
203071_at	SEMA3B	0.0018	-0.0242	0.0215	0.2637	0.0644	472 ± 63	647 ± 128	701 ± 107	1161 ± 327
203788_s_at	SEMA3C	0.0016	-0.0438	0.1701	-0.3260	0.0816	173 ± 14	191 ± 22	201 ± 12	277 ± 50
35666_at	SEMA3F	0.4129	-0.0220	-0.2913	0.4963	0.0729	520 ± 48	490 ± 68	469 ± 40	702 ± 93
46665_at	SEMA4C	0.0019	-0.0183	0.2363	-0.1388	0.0865	1383 ± 103	1781 ± 331	1934 ± 186	2537 ± 644
208124_s_at	SEMA4F	0.0145	-0.1111	0.1946	0.3547	0.4600	300 ± 14	298 ± 18	312 ± 12	346 ± 40
219194_at	SEMA4G	0.0297	-0.0307	0.0967	-0.0836	0.0678	403 ± 35	465 ± 49	457 ± 56	654 ± 112
215114_at	SENP3	0.0403	-0.1066	0.0943	-0.2966	0.3214	136 ± 14	167 ± 27	160 ± 27	194 ± 21
201427_s_at	SEPP1	0.6326	-0.0097	-0.1597	-0.1533	0.1292	7932 ± 1018	7599 ± 949	1772 ± 2027	1178 ± 1761
202376_at	SERPINA3	0.0641	-0.0200	-0.0574	0.4556	0.1254	4750 ± 1534	3185 ± 873	237 ± 2013	9225 ± 2380
213874_at	SERPINA4	0.0581	-0.0033	0.2556	0.4354	0.0087	170 ± 14	165 ± 26	206 ± 21	284 ± 35
210413_x_at	SERPINA4	0.3214	-0.0186	0.3165	-0.4704	0.0524	162 ± 12	152 ± 17	173 ± 20	244 ± 39
200986_at	SERPING1	0.8450	-0.0262	-0.2840	-0.2578	0.0455	406 ± 57	377 ± 48	364 ± 43	565 ± 34
207636_at	SERPIN2	0.0008	-0.0082	0.1503	-0.1183	0.0534	158 ± 17	179 ± 34	202 ± 24	273 ± 42
213048_s_at	SET	0.0357	-0.0450	0.2813	-0.0092	0.2526	2167 ± 202	2368 ± 346	2853 ± 265	2679 ± 214
37482_l_at	SF3A2	0.1671	-0.0295	0.0846	0.3454	0.1721	480 ± 33	570 ± 73	559 ± 39	669 ± 80
203818_s_at	SF3A3	0.0254	-0.0031	0.2043	-0.2822	0.0166	500 ± 21	518 ± 19	521 ± 21	595 ± 18
200688_at	SF3B3	0.0050	-0.0650	0.2027	0.1853	0.1305	479 ± 37	473 ± 46	539 ± 41	609 ± 50
33322_l_at	SFN	0.0105	-0.0004	0.2461	-0.0059	0.0000	949 ± 44	1154 ± 24	1026 ± 46	1571 ± 140
202035_s_at	SFRP1	0.0007	-0.0031	0.0197	-0.0105	0.0265	47 ± 5	70 ± 8	71 ± 6	95 ± 19
204051_s_at	SFRP4	0.3782	-0.0463	0.1317	-0.2424	0.4631	213 ± 26	215 ± 22	241 ± 14	259 ± 20
202775_s_at	SFRS8	0.0646	-0.0284	0.2639	0.1393	0.0695	995 ± 57	970 ± 98	1035 ± 124	1449 ± 215
38691_s_at	SFTPC	0.0087	-0.0129	0.1265	-0.1077	0.0249	421 ± 45	612 ± 70	580 ± 76	771 ± 114
201739_at	SGK	0.5440	-0.0260	-0.2537	-0.0234	0.2301	3269 ± 434	3649 ± 399	4770 ± 682	4333 ± 684
220357_s_at	SGK2	0.1788	-0.0397	0.0204	0.4107	0.0981	263 ± 11	335 ± 55	304 ± 26	400 ± 55
212321_at	SGPL1	0.0111	0.0000	0.2744	-0.1147	0.0021	489 ± 37	555 ± 42	668 ± 30	723 ± 61
201396_s_at	SGT	0.0021	-0.0531	0.0538	0.3991	0.1722	324 ± 21	365 ± 83	391 ± 45	552 ± 120
209370_s_at	SH3BP2	0.0090	-0.0046	0.2362	-0.3518	0.0243	318 ± 40	417 ± 56	571 ± 64	778 ± 192
205636_at	SH3GL3	0.0211	-0.0303	0.4552	0.1000	0.0247	222 ± 19	193 ± 16	209 ± 23	362 ± 75
46323_at	SHAPY	0.0144	-0.0552	0.2770	0.3441	0.1703	472 ± 25	479 ± 27	521 ± 27	550 ± 25
201956_s_at	SHARP	0.0089	-0.0115	-0.2994	-0.1248	0.0238	233 ± 26	238 ± 19	276 ± 23	357 ± 44
214853_s_at	SHC1	0.2562	-0.0371	-0.3108	0.2533	0.0865	1057 ± 105	786 ± 51	1094 ± 97	1239 ± 156

Web Table 5 (32)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
221519_at	SHFM3	split hand/foot malformation type 3	0.0116	-0.0068	0.0149	-0.1847	0.0400	1267 ± 89	1570 ± 221	1781 ± 166	1963 ± 217
214096_s_at	SHMT2	serine hydroxymethyltransferase 2	0.0171	-0.2061	0.4016	0.4485	0.4974	887 ± 59	857 ± 35	1000 ± 84	1020 ± 133
203759_at	SIAT4C	siatyltransferase 4C	0.0119	-0.0034	0.2510	-0.1040	0.0158	162 ± 17	172 ± 23	256 ± 21	270 ± 45
220937_s_at	SIAT7D	siatyltransferase	0.4560	-0.0035	0.0278	-0.0050	0.0731	99 ± 8	109 ± 11	112 ± 7	130 ± 6
210073_at	SIAT8A	siatyltransferase 8A	0.0492	-0.3977	-0.3620	0.3443	0.5285	131 ± 13	116 ± 12	144 ± 18	146 ± 18
213485_s_at	SIMRP7	multidrug resistance-associated protein 7	0.0175	-0.2048	0.1870	-0.4495	0.4536	763 ± 75	878 ± 166	886 ± 59	1030 ± 157
220605_s_at	SIRT2	sirtuin silent mating type information regulation 2 homolog 2	0.0142	-0.0951	-0.2493	0.3597	0.3275	1964 ± 166	2090 ± 184	2263 ± 191	2694 ± 527
219613_s_at	SIRT6	sirtuin silent mating type information regulation 2 homolog 6	0.1807	-0.0189	-0.0146	-0.4220	0.0150	343 ± 44	300 ± 49	315 ± 12	490 ± 45
218797_s_at	SIRT7	sirtuin silent mating type information regulation 2 homolog 7	0.0161	-0.0018	-0.3114	-0.1519	0.0416	352 ± 39	362 ± 31	422 ± 33	486 ± 34
202782_s_at	SKIP	skeletal muscle and kidney enriched histone phosphatase	0.6078	-0.0005	0.0337	-0.0870	0.0078	568 ± 24	568 ± 35	575 ± 36	720 ± 25
214734_at	SLC2-B	SLC2-B	0.0024	-0.0017	-0.4069	-0.2589	0.0025	374 ± 45	433 ± 30	428 ± 28	624 ± 66
206181_at	SLAM	signaling lymphocytic activation molecule	0.2031	-0.0004	0.0027	-0.1306	0.0083	86 ± 8	127 ± 17	125 ± 11	164 ± 20
217507_at	SLC11A1	solute carrier family 11, member 1	0.1333	-0.0248	0.3909	0.0671	0.0028	64 ± 13	88 ± 26	37 ± 8	182 ± 43
218274_at	SLC12A3	solute carrier family 12, member 3	0.1475	-0.0066	0.2175	-0.0172	0.0233	140 ± 14	174 ± 11	177 ± 25	250 ± 39
218066_at	SLC12A7	solute carrier family 12, member 7	0.0825	-0.0001	0.0797	-0.0827	0.0015	807 ± 80	842 ± 93	929 ± 79	1489 ± 99
220502_s_at	SLC13A1	solute carrier family 13, member 1	0.2660	-0.0168	-0.4419	0.3546	0.0951	17 ± 4	20 ± 5	31 ± 1	39 ± 9
205856_at	SLC14A1	solute carrier family 14, member 1	0.0048	-0.0001	0.0407	-0.4844	0.0056	430 ± 69	517 ± 38	701 ± 91	1329 ± 326
211576_s_at	SLC19A1	solute carrier family 19, member 1	0.0195	0.0000	0.0320	-0.0004	0.0007	209 ± 19	287 ± 25	344 ± 26	426 ± 52
210923_at	SLC17	solute carrier family 1, member 7	0.0137	-0.0283	-0.2105	-0.3714	0.1233	295 ± 23	326 ± 41	301 ± 18	415 ± 46
219229_at	SLC21A11	solute carrier family 21, member 11	0.0456	-0.0097	-0.2451	0.4273	0.1721	365 ± 43	389 ± 35	523 ± 75	493 ± 47
210010_s_at	SLC25A1	solute carrier family 25, member 1	0.0499	-0.0323	0.4538	-0.4170	0.0470	494 ± 61	549 ± 79	623 ± 41	762 ± 147
220474_at	SLC25A21	solute carrier family 25, member 21	-0.9853	-0.0327	-0.1505	-0.1534	0.5196	19 ± 5	23 ± 5	46 ± 11	42 ± 7
205097_at	SLC26A2	solute carrier family 26, member 2	0.0052	-0.0049	-0.0903	-0.4792	0.0369	197 ± 32	203 ± 17	232 ± 24	251 ± 36
204717_s_at	SLC29A2	solute carrier family 29, member 2	0.3114	-0.0368	0.4063	0.4693	0.1211	95 ± 12	80 ± 15	133 ± 23	182 ± 42
201250_s_at	SLC2A1	solute carrier family 2, member 1	0.0063	-0.0954	0.1320	0.3725	0.1217	1655 ± 125	1782 ± 270	1626 ± 73	2257 ± 279
218494_s_at	SLC2A4RG	SLC2A4 regulator	0.0184	-0.0070	0.1222	0.4332	0.0006	236 ± 21	279 ± 32	312 ± 30	337 ± 41
219991_at	SLC2A9	solute carrier family 2, member 9	0.0249	-0.0186	0.1983	-0.4383	0.0232	363 ± 28	432 ± 44	370 ± 21	601 ± 58
207440_at	SLC35A2	solute carrier family 35, member 2	0.0515	-0.0134	0.0066	-0.0023	0.0002	110 ± 15	160 ± 23	188 ± 9	199 ± 34
209665_at	SLC35A3	solute carrier family 35, transporter, member 3	0.0160	-0.0633	0.2943	-0.1262	0.2556	78 ± 7	158 ± 10	140 ± 13	156 ± 15
218237_s_at	SLC38A1	solute carrier family 38, member 1	0.0323	-0.0614	0.1752	-0.1081	0.1841	1248 ± 44	1430 ± 134	1427 ± 134	1595 ± 143
210739_x_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter 4	0.4631	-0.0233	0.2789	-0.0568	0.1319	692 ± 39	701 ± 42	739 ± 54	973 ± 193
209884_s_at	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter 7	0.0049	-0.0103	-0.3691	-0.4310	0.0399	206 ± 19	242 ± 23	268 ± 28	298 ± 41
210854_x_at	SLC6A8	solute carrier family 6, member 8	0.0000	-0.0011	0.3759	-0.0785	0.0160	703 ± 48	654 ± 36	774 ± 37	874 ± 72
201195_s_at	SLC7A5	solute carrier family 7, member 5	0.0120	-0.0325	0.1937	-0.4160	0.0275	188 ± 11	164 ± 18	212 ± 20	285 ± 46
203579_s_at	SLC7A6	solute carrier family 7, member 6	0.0068	-0.0275	0.3509	-0.3496	0.0523	164 ± 26	196 ± 26	205 ± 22	298 ± 57
208039_at	SLC9A2	solute carrier family 9, isoform 2	0.0460	-0.0917	0.0925	-0.0662	0.2044	1396 ± 72	1624 ± 80	1750 ± 114	1717 ± 211
206874_s_at	SLK	Slk20-related serine/threonine kinase	0.0021	-0.0652	0.1644	-0.1777	0.1696	225 ± 36	312 ± 49	414 ± 92	535 ± 184
214850_at	SMA3	SMA3	0.0066	-0.0286	0.0725	0.4557	0.2346	322 ± 52	563 ± 158	987 ± 351	791 ± 317
215599_at	SMA4	SMA4	0.0162	-0.1204	-0.2783	-0.0310	0.4058	248 ± 36	293 ± 41	338 ± 19	319 ± 62
201073_s_at	SMARCC1	actin dependent regulator of chromatin, subfamily c, member 1	0.0011	-0.0747	0.3060	-0.0167	0.0463	932 ± 107	1146 ± 57	1502 ± 98	1293 ± 259
201320_at	SMARCC2	actin dependent regulator of chromatin, subfamily c, member 2	0.2408	-0.0094	0.3760	0.3416	0.0334	269 ± 21	253 ± 27	313 ± 23	390 ± 51
203183_s_at	SMARCD1	actin dependent regulator of chromatin, subfamily d, member 1									

Web Table 5 (33)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
212152_x_at	SMARCF1	0.0206	-0.0483	0.2636	-0.0423	0.0443	1942 ± 116	2278 ± 95	2366 ± 123	2341 ± 130
201589_at	SMC1L1	0.3775	-0.0049	0.2678	-0.0381	0.1786	620 ± 69	730 ± 100	824 ± 99	873 ± 78
215823_x_at	SMC4L1	0.9070	-0.0084	0.2051	-0.3477	0.0209	47 ± 5	54 ± 4	48 ± 9	84 ± 13
200739_s_at	SMT3H1	0.0229	-0.4166	0.3982	-0.1993	0.3171	227 ± 18	238 ± 28	222 ± 17	315 ± 72
213139_at	SNAI2	0.1765	-0.0319	0.4459	-0.1751	0.3069	67 ± 8	67 ± 16	79 ± 10	97 ± 13
205443_at	SNAPC1	0.0258	-0.3086	0.0079	0.0182	0.2461	99 ± 12	79 ± 10	106 ± 8	116 ± 17
204104_at	SNAPC2	0.0102	-0.0008	0.3018	0.1674	0.0007	158 ± 10	170 ± 15	262 ± 21	263 ± 33
207474_at	SNRK	0.6988	-0.0487	0.0826	-0.0033	0.3816	60 ± 12	79 ± 12	76 ± 10	95 ± 26
201221_s_at	SNRP70	0.0151	-0.0709	0.3048	0.3104	0.0651	2083 ± 140	2283 ± 358	2252 ± 288	3607 ± 741
203516_at	SNTA1	0.0048	-0.0674	0.1956	0.3795	0.0179	1068 ± 93	1166 ± 167	1772 ± 126	1439 ± 259
220140_s_at	SNX11	0.0211	-0.0482	0.0089	-0.2493	0.0174	436 ± 36	594 ± 52	537 ± 52	646 ± 34
219793_at	SNX16	0.0177	-0.0954	0.3075	-0.0032	0.3081	72 ± 8	89 ± 14	101 ± 8	97 ± 16
217789_at	SNX6	0.0032	-0.0871	0.2358	-0.3492	0.2253	578 ± 53	770 ± 117	861 ± 96	963 ± 226
215078_at	SOD2	0.2895	-0.0120	0.4533	0.1783	0.1261	32 ± 7	43 ± 6	52 ± 10	68 ± 16
204275_at	SOLH	0.0498	-0.2702	0.2357	-0.2695	0.2524	247 ± 20	232 ± 11	309 ± 18	276 ± 44
218087_s_at	SORBS1	0.0146	-0.0500	0.1955	-0.0631	0.0032	3538 ± 296	3953 ± 332	6032 ± 568	4431 ± 613
201563_at	SORD	0.0355	-0.0005	0.4184	-0.1133	0.0256	384 ± 37	435 ± 44	519 ± 52	575 ± 48
204432_at	SOX12	0.0323	-0.1077	0.4298	-0.2083	0.3770	179 ± 20	195 ± 23	249 ± 36	241 ± 51
38918_at	SOX13	0.0671	-0.0135	0.4324	-0.2430	0.0320	224 ± 23	245 ± 13	309 ± 10	283 ± 27
213721_at	SOX2	0.0051	-0.0886	0.2700	-0.3085	0.2874	911 ± 63	1027 ± 120	1106 ± 93	1159 ± 107
202935_s_at	SOX9	0.2072	-0.0413	0.4124	-0.1193	0.3201	1868 ± 242	1947 ± 226	2225 ± 200	2432 ± 256
202863_at	SP100	0.4149	-0.0013	0.3967	-0.3193	0.0095	201 ± 17	207 ± 12	204 ± 22	306 ± 37
209761_s_at	SP110	0.0074	-0.0083	0.3462	-0.2521	0.0630	291 ± 33	323 ± 20	381 ± 33	442 ± 66
213168_at	SP3	0.4829	-0.0184	0.3456	-0.0029	0.1453	1082 ± 49	1073 ± 103	1305 ± 74	1185 ± 103
210117_at	SPAG1	0.0113	0.0000	0.0028	-0.0951	0.0005	108 ± 9	143 ± 21	142 ± 13	215 ± 18
210033_s_at	SPAG6	0.2245	-0.0057	0.1899	0.4068	0.0009	140 ± 15	134 ± 5	124 ± 26	248 ± 21
212468_at	SPAG9	0.3476	-0.0233	0.0609	-0.0580	0.1248	297 ± 30	387 ± 38	405 ± 32	422 ± 59
200865_s_at	SPARC	0.0672	-0.0003	0.1639	-0.1010	0.0226	2913 ± 418	2830 ± 596	3905 ± 516	5716 ± 1081
201290_at	SPC18	0.0088	-0.0240	0.2285	-0.1576	0.0671	1337 ± 91	1513 ± 121	1742 ± 101	1654 ± 144
219257_s_at	SPHK1	0.1330	-0.0402	0.2498	-0.2398	0.1792	211 ± 31	277 ± 24	271 ± 29	302 ± 31
205861_at	SPIB	0.0362	-0.0016	0.4522	-0.0102	0.0071	145 ± 14	150 ± 23	153 ± 16	241 ± 29
204640_s_at	SPOP	0.0130	-0.0508	0.3502	-0.2411	0.0513	1577 ± 128	1574 ± 47	1983 ± 71	1808 ± 165
208939_at	SPS	0.0076	0.0000	0.3770	-0.1017	0.0019	613 ± 30	654 ± 55	762 ± 39	930 ± 91
203127_s_at	SPTLC2	0.3684	-0.0010	0.0919	-0.3287	0.0036	448 ± 40	418 ± 46	407 ± 30	670 ± 76
214072_x_at	SPUF	0.5587	-0.0258	0.0221	-0.0119	0.0605	260 ± 12	331 ± 28	294 ± 19	340 ± 27
38766_at	SRAP	0.0051	-0.0128	0.3534	-0.4363	0.0079	262 ± 30	364 ± 39	396 ± 17	446 ± 48
202308_at	SREBF1	0.0167	-0.0249	0.0002	-0.1787	0.0319	526 ± 42	967 ± 130	858 ± 105	1198 ± 268
201248_s_at	SREBF2	0.0109	-0.0222	0.3194	-0.3374	0.0764	514 ± 47	482 ± 23	647 ± 56	717 ± 112
203181_x_at	SRPK2	0.0024	-0.0078	0.2557	-0.0210	0.0249	653 ± 49	780 ± 42	898 ± 72	902 ± 75
204955_at	SRPX	0.0329	-0.0001	0.3611	-0.1210	0.0201	555 ± 67	603 ± 91	759 ± 104	1030 ± 163
208610_s_at	SRRM2	0.1392	-0.0188	0.1935	-0.1035	0.1846	922 ± 118	1020 ± 111	1178 ± 148	1420 ± 249
219405_at	SS-56	0.3120	-0.0186	0.1404	-0.1418	0.2804	340 ± 33	345 ± 25	374 ± 17	411 ± 29

Web Table 5 (34)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
212852_s_at	SSA2	Sjogren syndrome antigen A2	0.0009	-0.0134	0.1610	-0.4100	0.0711	1973 ± 193	2150 ± 259	2577 ± 178	2909 ± 392
46256_at	SSB-3	Sjogren syndrome antigen B3	0.0081	-0.0069	0.4760	0.1705	0.0072	1667 ± 47	1832 ± 250	1808 ± 44	2744 ± 389
202506_at	SSFA2	sperm specific antigen 2	0.0486	-0.0010	0.4770	-0.0126	0.0542	893 ± 105	1059 ± 103	1376 ± 188	1419 ± 174
221753_at	SSH1	slingshot 1	0.0640	-0.0177	0.1460	-0.0289	0.0711	355 ± 25	388 ± 18	427 ± 31	479 ± 50
51192_at	SSH-3	slingshot 3	0.0014	-0.0009	0.0268	-0.3388	0.0044	291 ± 21	370 ± 27	393 ± 23	619 ± 115
214105_at	SSI-3	suppressor of cytokine signaling 3	0.0025	-0.0095	0.4300	0.2982	0.0089	40 ± 5	42 ± 8	89 ± 7	107 ± 29
204964_s_at	SSPN	sarcomer	0.1982	-0.0037	0.3021	-0.0074	0.0230	285 ± 38	362 ± 66	426 ± 51	576 ± 98
200652_at	SSR2	signal sequence receptor, β	0.0403	-0.0540	0.0499	-0.2850	0.0660	1023 ± 47	1151 ± 63	1115 ± 26	1269 ± 101
202440_s_at	ST5	suppression of tumorigenicity 5	0.0393	-0.0180	0.2207	0.4519	0.0906	379 ± 36	336 ± 40	464 ± 35	471 ± 46
202294_at	STAG1	stromal antigen 1	0.0723	-0.0294	-0.1990	0.4287	0.0288	565 ± 30	568 ± 73	588 ± 27	793 ± 86
203023_s_at	STAG2	stromal antigen 2	0.0027	-0.0085	0.3459	-0.0066	0.0240	506 ± 61	644 ± 21	837 ± 75	757 ± 22
202991_at	STARD3	START domain containing 3	0.0225	-0.1621	-0.3479	0.3569	0.4592	195 ± 15	194 ± 21	241 ± 33	241 ± 33
201331_s_at	STAT6	signal transducer and activator of transcription 6	0.0223	-0.0179	0.4762	-0.3917	0.1537	618 ± 51	569 ± 29	640 ± 43	760 ± 88
213037_x_at	STAU	stauflin, RNA binding protein	0.1214	-0.0495	-0.0476	-0.1455	0.0939	3023 ± 133	2850 ± 66	3353 ± 116	3251 ± 204
202764_at	STIM1	stromal interaction molecule 1	0.0215	-0.0026	0.0697	-0.1609	0.0654	253 ± 28	255 ± 23	324 ± 17	338 ± 33
40420_at	STK10	serine/threonine kinase 10	0.1280	-0.0092	0.1361	-0.1559	0.0553	223 ± 20	253 ± 28	240 ± 13	310 ± 26
41657_at	STK11	serine/threonine kinase 11	0.0944	-0.0050	0.1801	0.0657	0.0056	806 ± 99	738 ± 104	891 ± 35	1421 ± 15
212565_at	STK38L	serine/threonine kinase 38 like	0.2831	-0.0388	-0.2267	-0.3637	0.1654	494 ± 37	429 ± 52	515 ± 9	582 ± 66
203330_s_at	STX5A	syntaxin 5A	0.3823	-0.0434	0.1426	-0.0747	0.1213	180 ± 17	229 ± 15	210 ± 20	247 ± 7
215588_x_at	SUDD	sudD suppressor of bimD6 homolog	0.0036	-0.0364	0.1992	-0.1362	0.1386	1815 ± 216	1913 ± 136	2669 ± 330	3159 ± 836
206593_s_at	SURF5	surfeit 5	0.4824	-0.0229	0.0728	-0.1322	0.3090	393 ± 26	398 ± 37	439 ± 21	468 ± 36
219262_at	SUV39H2	suppressor of variegation 3-9 homolog 2	0.6039	-0.0475	0.2314	-0.4013	0.0841	39 ± 5	39 ± 10	41 ± 10	74 ± 17
204978_at	SWAP2	suppressor of white apricot homolog 2	0.0017	-0.0242	0.2863	-0.4042	0.0522	949 ± 115	1131 ± 161	1135 ± 118	1803 ± 405
206546_at	SYCP2	synaptonemal complex protein 2	0.0032	-0.0905	0.0001	-0.0670	0.2322	32 ± 3	45 ± 7	53 ± 7	55 ± 15
221276_s_at	SYNCOILIN	intermediate filament protein syncoilin	0.0021	-0.0021	0.3414	-0.0113	0.0160	119 ± 12	126 ± 22	165 ± 21	198 ± 18
221898_at	T1A-2	lung type-I cell membrane-associated glycoprotein	0.4797	-0.0091	-0.2149	-0.3009	0.1723	174 ± 32	143 ± 16	209 ± 17	232 ± 38
217437_s_at	TACC1	transforming, acidic coiled-coil containing protein 1	0.2180	-0.0049	0.0210	-0.2360	0.1797	458 ± 23	501 ± 27	555 ± 54	612 ± 79
215272_at	TADA3L	transcriptional adaptor 3-like	0.0400	-0.1427	0.4103	-0.4306	0.3476	79 ± 12	73 ± 18	82 ± 12	124 ± 38
209358_at	TAF11	TAF11 RNA polymerase II	0.0573	-0.0316	0.1939	-0.4966	0.0756	458 ± 39	485 ± 40	479 ± 38	613 ± 55
202840_at	TAF15	TAF15 RNA polymerase II	0.0532	-0.0073	0.0564	-0.0856	0.0382	351 ± 34	350 ± 32	504 ± 33	489 ± 77
210053_at	TAF5	TAF5 RNA polymerase II	0.0976	-0.0345	-0.2634	-0.2789	0.1180	321 ± 25	306 ± 36	398 ± 26	376 ± 34
205547_s_at	TAGLN	transgelin	0.0000	-0.0120	0.1651	-0.2519	0.0289	225 ± 31	239 ± 37	341 ± 22	362 ± 54
204877_s_at	TAO1	thousand and one amino acid protein kinase	0.6842	-0.0399	0.0067	0.3208	0.0183	114 ± 10	122 ± 9	97 ± 7	180 ± 33
20307_s_at	TAP1	transporter 1, ATP-binding cassette, sub-family B	0.7251	-0.0383	0.1327	-0.3236	0.1894	385 ± 48	418 ± 76	338 ± 42	653 ± 200
208829_at	TAPBP	TAP binding protein	0.0159	-0.1026	0.4846	-0.1862	0.0695	1245 ± 102	1233 ± 54	1582 ± 115	1433 ± 109
206916_x_at	TAT	taste receptor, type 2, member 16	0.3909	-0.0196	0.1102	-0.2086	0.0559	146 ± 14	162 ± 15	152 ± 15	210 ± 23
202133_at	TAZ	tyrosine aminotransferase	0.0666	-0.0279	-0.2050	-0.3071	0.0128	59 ± 11	52 ± 5	55 ± 9	105 ± 16
222173_s_at	TBC1D2	transcriptional co-activator with PDZ-binding motif	0.0991	-0.0399	0.1714	-0.0474	0.0029	475 ± 84	634 ± 95	1340 ± 265	912 ± 106
201813_s_at	TBC1D5	TBC1 domain family, member 2	0.0284	-0.0129	0.0340	-0.3220	0.0371	88 ± 18	66 ± 22	55 ± 11	160 ± 45
213400_s_at	TBL1X	TBC1 domain family, member 5	0.0024	-0.0002	0.2245	-0.0342	0.0431	776 ± 19	890 ± 45	925 ± 74	1062 ± 103
215122_at	TBX6	transducin-like 1X-linked T-box 6	0.0593	-0.0294	-0.2407	-0.0532	0.0007	853 ± 75	949 ± 126	1106 ± 68	1624 ± 196

Web Table 5 (35)

Probe set Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
207554_x_at	thromboxane A2 receptor	0.3649	-0.0094	0.0037	-0.1471	0.0080	171 ± 19	203 ± 20	171 ± 21	284 ± 35
212122_at	ras-like protein TC10	0.0055	-0.0006	0.0599	-0.0001	0.0012	154 ± 17	247 ± 26	292 ± 20	280 ± 36
212931_at	transcription factor 20	0.0210	-0.4521	-0.4258	0.1709	0.2903	870 ± 25	848 ± 79	1067 ± 63	979 ± 158
209153_s_at	transcription factor 3	0.0003	-0.0005	0.1557	-0.0216	0.0089	224 ± 32	293 ± 34	438 ± 66	468 ± 72
221016_s_at	HMG-box transcription factor TCF-3	0.0004	-0.0048	0.1881	-0.1469	0.0108	355 ± 24	444 ± 45	455 ± 37	563 ± 51
205255_x_at	transcription factor 7	0.0052	-0.0263	0.1623	-0.4557	0.0352	804 ± 96	1143 ± 180	970 ± 104	1628 ± 325
212761_at	transcription factor 7-like 2	0.0147	-0.0006	0.1012	-0.3033	0.0261	1861 ± 116	2134 ± 213	2302 ± 127	2883 ± 396
204043_at	transcobalamin II; macrocytic anemia	0.4467	-0.0281	0.0083	-0.0053	0.0877	239 ± 16	320 ± 30	293 ± 32	345 ± 41
202384_s_at	Treacher Collins-Franceschetti syndrome 1	0.0040	-0.1318	0.4932	-0.0009	0.0595	150 ± 14	177 ± 18	268 ± 38	205 ± 44
201999_s_at	t-complex-associated-testis-expressed 1-like 1	0.0401	-0.0003	-0.1117	-0.1475	0.0192	1062 ± 71	1086 ± 66	1309 ± 108	1498 ± 154
203742_s_at	thymine-DNA glycosylase	0.0043	-0.0134	-0.0481	-0.3433	0.0227	181 ± 19	158 ± 6	194 ± 14	287 ± 55
201737_s_at	similar to S. cerevisiae SSM4	0.0373	-0.0279	0.2946	-0.0212	0.0551	1927 ± 111	2131 ± 127	2717 ± 277	2452 ± 714
200804_at	testis enhanced gene transcript	0.0924	-0.0081	0.2297	-0.0781	0.0132	5273 ± 269	5521 ± 350	6661 ± 244	6016 ± 364
221880_s_at	transcription factor eis	0.0211	-0.0004	0.1299	-0.1338	0.0126	145 ± 12	176 ± 10	211 ± 21	240 ± 29
219025_at	tumor endothelial marker 1 precursor	0.0036	-0.0122	-0.4062	-0.1802	0.0713	280 ± 24	301 ± 7	352 ± 47	451 ± 77
217853_at	tumor endothelial marker 6	0.1228	-0.0027	0.0146	-0.2218	0.0210	2462 ± 159	2999 ± 448	4169 ± 468	4407 ± 725
220147_s_at	TERA protein	0.1892	-0.0370	-0.1013	-0.2693	0.2641	428 ± 43	460 ± 21	458 ± 30	530 ± 40
202720_at	testis derived transcript	0.4626	-0.0111	0.4356	-0.1491	0.0955	215 ± 34	199 ± 43	225 ± 27	321 ± 33
218020_s_at	testis expressed sequence 27	0.3407	-0.0397	-0.4504	0.3833	0.1559	1007 ± 52	1111 ± 69	1120 ± 57	1210 ± 71
214063_s_at	transferrin	0.1738	-0.0017	0.4695	-0.0883	0.0396	6535 ± 841	6388 ± 707	1136 ± 1103	1139 ± 1856
204653_at	transcription factor AP-2 α	0.3762	-0.0453	-0.1267	0.3997	0.0021	125 ± 20	109 ± 17	85 ± 17	218 ± 34
212457_at	transcription factor binding to IGHM enhancer 3	0.0362	-0.1708	-0.0995	-0.2453	0.0150	1132 ± 81	937 ± 92	1393 ± 111	1134 ± 58
50221_at	transcription factor EB	0.0654	-0.0085	0.1780	-0.4414	0.1582	677 ± 82	790 ± 133	891 ± 123	1170 ± 249
208715_at	transcription factor EC	0.0705	-0.0235	-0.4850	-0.0634	0.0440	72 ± 13	87 ± 13	78 ± 10	123 ± 13
203085_s_at	transforming growth factor, β 1	0.3127	-0.0033	0.2759	0.4450	0.0134	402 ± 33	364 ± 16	406 ± 47	644 ± 107
209651_at	transforming growth factor β 1 induced transcript 1	0.0569	-0.0001	0.1423	-0.3400	0.0016	256 ± 29	257 ± 32	351 ± 30	515 ± 76
209909_s_at	transforming growth factor, β 2	0.0458	-0.0137	-0.2768	-0.0691	0.0277	57 ± 6	52 ± 10	66 ± 9	95 ± 15
204731_at	transforming growth factor, β receptor III	0.0048	-0.0001	0.3427	-0.0168	0.0091	339 ± 33	413 ± 40	512 ± 66	630 ± 87
203313_s_at	TGFB-induced factor	0.1384	-0.0076	-0.0130	0.1977	0.0637	204 ± 31	160 ± 11	275 ± 22	298 ± 62
216262_s_at	TGFB-induced factor 2	0.3764	-0.0102	0.2323	-0.0885	0.0367	200 ± 24	229 ± 22	197 ± 14	295 ± 36
212596_s_at	partial transcript encompassing THC211630 gene	0.0016	-0.1049	0.2030	0.3692	0.2414	575 ± 47	640 ± 100	767 ± 109	951 ± 247
208104_s_at	TSC-22-like	0.0397	-0.0213	0.0196	-0.0480	0.0386	730 ± 59	968 ± 139	1231 ± 136	1097 ± 142
222122_s_at	Tho2	0.0404	-0.0989	0.4113	-0.0364	0.2425	398 ± 39	377 ± 36	369 ± 29	470 ± 38
1316_at	thyroid hormone receptor, α oncogene homolog, avian	0.0787	-0.0041	0.1177	-0.1348	0.0089	161 ± 10	200 ± 19	204 ± 18	278 ± 36
202039_at	TGFB1-induced anti-apoptotic factor 1	0.0012	-0.0569	0.1168	-0.3206	0.1704	1417 ± 134	1796 ± 259	2099 ± 192	2348 ± 562
203317_at	SEC7 homolog	0.0203	-0.0014	0.0514	0.3490	0.0044	78 ± 17	94 ± 10	173 ± 19	172 ± 33
204391_x_at	transcriptional intermediary factor 1	0.0019	-0.0483	-0.0013	0.0578	0.1005	485 ± 13	469 ± 49	558 ± 39	611 ± 62
203046_s_at	timeless homolog	0.0374	-0.0640	-0.3186	-0.0681	0.1319	172 ± 20	240 ± 38	208 ± 16	284 ± 55
203093_s_at	translocase of inner mitochondrial membrane 44 homolog	0.0215	-0.0010	0.2759	0.0405	0.0199	221 ± 8	232 ± 26	276 ± 18	356 ± 56
209154_at	Tax interaction protein 1	0.0516	-0.0025	0.0013	-0.0847	0.0353	1652 ± 192	2510 ± 446	2896 ± 347	3486 ± 649
202122_s_at	cargo selection protein	0.0586	-0.0315	0.3834	-0.4372	0.2473	585 ± 82	743 ± 105	825 ± 87	953 ± 110
217367_s_at	triple homeobox 1	0.0000	0.0000	0.0370	-0.0144	0.0001	511 ± 47	593 ± 47	761 ± 57	913 ± 74

Web Table 5 (36)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
202085_at	TJP2	tight junction protein 2	0.0172	-0.0007	-0.4256	-0.0691	0.0605	1428 ± 145	1570 ± 296	1904 ± 182	2266 ± 271
47608_at	TJP4	tight junction protein 4	0.0064	-0.0907	0.1283	-0.1933	0.2218	1175 ± 140	1563 ± 222	1462 ± 164	1948 ± 458
212769_at	TLE3	transducin-like enhancer of split 3 homolog	0.0083	-0.0002	0.0571	-0.1175	0.0016	90 ± 8	86 ± 7	135 ± 13	141 ± 10
214688_at	TLE4	transducin-like enhancer of split 4 homolog	0.1134	-0.0428	-0.4730	-0.3002	0.0285	121 ± 10	123 ± 10	107 ± 16	179 ± 26
206415_at	TLL1	toll-like 1	0.0503	-0.0293	0.0840	-0.3975	0.0103	32 ± 3	28 ± 5	33 ± 5	67 ± 15
208942_s_at	TLOC1	translocation protein 1	0.0074	-0.1167	0.4150	-0.2947	0.0269	2138 ± 96	2214 ± 163	2738 ± 172	2411 ± 124
210176_at	TLR1	toll-like receptor 1	0.0766	-0.0018	-0.3761	-0.0390	0.0162	71 ± 9	93 ± 16	100 ± 4	126 ± 7
209108_at	TM4SF6	transmembrane 4 superfamily member 6	0.2463	-0.0003	-0.3779	-0.1027	0.0075	526 ± 47	518 ± 40	616 ± 78	881 ± 111
217974_at	TM7SF3	seven transmembrane protein TM7SF3	-0.8483	-0.0293	-0.4844	-0.0116	0.4008	159 ± 16	146 ± 22	164 ± 19	193 ± 19
221882_s_at	TMEM8	transmembrane protein 8	0.0232	-0.5294	0.0337	-0.4415	0.5615	147 ± 13	174 ± 33	198 ± 35	221 ± 69
220177_s_at	TMPRSS3	transmembrane protease, serine 3	0.2412	-0.0226	0.1712	-0.4257	0.0644	175 ± 16	147 ± 15	210 ± 20	229 ± 29
201645_at	TNC	tenascin C	0.2291	-0.0475	0.0459	-0.4827	0.0633	231 ± 46	284 ± 46	479 ± 100	393 ± 36
202644_s_at	TNFAIP3	tumor necrosis factor, α-induced protein 3	0.0177	-0.0070	0.0628	-0.3436	0.0137	289 ± 24	366 ± 30	335 ± 26	446 ± 45
209295_at	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	0.9726	-0.0366	-0.2500	0.2795	0.3513	385 ± 36	352 ± 21	396 ± 44	476 ± 78
204932_at	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	0.0240	-0.0018	0.0407	-0.1543	0.0031	48 ± 4	59 ± 6	74 ± 12	105 ± 16
207643_s_at	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	0.0207	-0.0163	0.0995	-0.4246	0.0240	563 ± 44	743 ± 72	700 ± 72	895 ± 90
207536_s_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	0.0028	-0.0428	0.0490	0.4553	0.0101	116 ± 8	173 ± 26	146 ± 7	239 ± 42
202687_s_at	TNFSF10	tumor necrosis factor superfamily, member 10	0.0134	-0.2852	0.2810	-0.2411	0.3852	50 ± 9	69 ± 9	70 ± 15	91 ± 27
217931_at	TNRC5	trinucleotide repeat containing 5	0.0064	-0.0369	0.0095	-0.1251	0.0788	237 ± 16	312 ± 37	308 ± 23	403 ± 75
216333_x_at	TNXB	tenascin XB	0.0002	-0.0121	0.0109	-0.0060	0.0003	163 ± 24	236 ± 47	451 ± 47	332 ± 55
222243_s_at	TOB2	transducer of ERBB2, 2	0.0020	-0.0011	-0.3341	-0.0540	0.0476	794 ± 106	881 ± 108	1132 ± 74	1189 ± 153
202807_s_at	TOM1	target of myb1	0.0059	-0.0865	0.1112	-0.2997	0.0236	255 ± 22	230 ± 20	376 ± 22	316 ± 59
204946_s_at	TOP3A	topoisomerase III α	0.0429	-0.3092	0.1462	-0.3943	0.3966	371 ± 38	471 ± 76	398 ± 46	523 ± 111
201746_at	TP53	tumor protein p53	0.0053	-0.0211	0.1652	-0.3715	0.0912	166 ± 20	203 ± 27	238 ± 26	265 ± 41
204071_s_at	TP53BPL	tumor protein p53-binding protein	0.0064	-0.0199	0.0400	-0.1030	0.0925	233 ± 9	264 ± 22	270 ± 29	324 ± 31
201691_s_at	TPD52	tumor protein D52	0.0017	-0.0030	0.0206	0.4724	0.0047	222 ± 19	263 ± 17	294 ± 28	362 ± 35
203786_s_at	TPD52L1	tumor protein D52-like 1	0.1937	-0.0273	-0.1000	-0.0374	0.1145	2979 ± 178	3119 ± 229	3012 ± 332	4117 ± 598
201379_s_at	TPD52L2	tumor protein D52-like 2	0.0048	-0.5364	0.2441	-0.4572	0.1182	652 ± 68	761 ± 109	980 ± 66	740 ± 161
203671_at	TPMT	thiopurine S-methyltransferase	0.1615	-0.0012	0.0561	-0.1834	0.0077	284 ± 36	322 ± 23	383 ± 20	469 ± 57
218855_at	TPRA40	seven transmembrane domain orphan receptor	0.0168	-0.2582	-0.2730	0.3201	0.4653	222 ± 16	237 ± 20	267 ± 21	268 ± 39
220865_s_at	TPT	trans-prenyltransferase	0.2911	-0.0165	0.0521	-0.0410	0.0691	264 ± 21	292 ± 19	278 ± 34	362 ± 27
211943_x_at	TPT1	tumor protein, translationally-controlled 1	0.1925	-0.0405	-0.0026	0.3018	0.1084	16377 ± 877	5133 ± 1005	1637 ± 1213	8266 ± 1229
220205_at	TPTE	transmembrane phosphatase with tensin homology	0.6237	-0.0317	0.0599	-0.2294	0.0731	38 ± 7	57 ± 11	49 ± 11	83 ± 18
201398_s_at	TRAM	translocating chain-associating membrane protein	0.3401	-0.0005	0.2403	-0.0534	0.0280	1596 ± 80	1807 ± 103	2141 ± 124	2218 ± 267
213043_s_at	TRAP100	thyroid hormone receptor-associated protein	0.0597	-0.0485	-0.2229	-0.4669	0.1912	591 ± 38	540 ± 17	624 ± 61	708 ± 65
201986_at	TRAP240	thyroid hormone receptor-associated protein	0.0027	-0.0063	0.3155	-0.1257	0.0475	1278 ± 74	1446 ± 109	1468 ± 90	1664 ± 99
213193_x_at	TRB	T cell receptor β locus	0.0254	-0.0319	0.0866	-0.1659	0.1197	328 ± 38	383 ± 51	377 ± 33	512 ± 88
34689_at	TREX1	three prime repair exonuclease 1	0.0831	-0.0176	0.1211	-0.0637	0.0251	759 ± 42	885 ± 59	870 ± 62	1069 ± 95
207891_s_at	TREX2	three prime repair exonuclease 2	0.0488	-0.0640	0.2984	-0.0508	0.3501	282 ± 29	344 ± 23	338 ± 32	397 ± 80
218425_at	TRIAD3	TRIAD3 protein	0.0203	-0.3308	0.0550	-0.0816	0.2094	340 ± 32	455 ± 41	486 ± 25	463 ± 97
210579_s_at	TRIM10	tripartite motif-containing 10	0.4299	-0.0071	0.0511	-0.0920	0.0176	91 ± 21	120 ± 16	83 ± 16	208 ± 49
203148_s_at	TRIM14	tripartite motif-containing 14	0.0169	-0.0057	0.0854	0.3826	0.0182	161 ± 17	220 ± 38	268 ± 22	342 ± 70

Web Table 5 (37)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
202702_at TRIM26	tripartite motif-containing 26	0.0738	-0.0002	0.3671	-0.2454	0.0008	447 ± 30	513 ± 16	468 ± 28	655 ± 51
203568_s_at TRIM38	tripartite motif-containing 38	0.3111	-0.0378	0.0073	-0.0026	0.3079	202 ± 19	264 ± 14	262 ± 41	292 ± 53
202734_at TRIP10	thyroid hormone receptor interactor 10	0.0172	-0.0498	0.3782	-0.3294	0.2308	428 ± 52	559 ± 97	590 ± 67	670 ± 122
203732_at TRIP4	thyroid hormone receptor interactor 4	0.1021	-0.0063	-0.2594	-0.0905	0.0025	398 ± 17	429 ± 33	366 ± 13	509 ± 30
202655_s_at TRIP-B2	transcriptional regulator interacting with the PHS-bromodomain	0.0002	0.0000	0.2766	-0.1218	0.0002	425 ± 26	477 ± 33	596 ± 38	670 ± 50
212318_at TRN-SR	transporin-SR	0.0078	-0.0136	0.2962	-0.2555	0.0367	757 ± 63	738 ± 39	964 ± 70	1083 ± 151
218502_s_at TRPS1	trichorhinophthalangeal syndrome 1	0.0169	-0.0163	0.1541	-0.3020	0.0692	666 ± 89	793 ± 117	1044 ± 137	998 ± 190
219632_s_at TRPV1	transient receptor potential cation channel V1	0.0073	-0.0696	0.1670	0.4987	0.0741	327 ± 34	420 ± 62	398 ± 32	592 ± 26
212689_s_at TSGA	zinc finger protein	0.0668	-0.0156	-0.3911	-0.2230	0.2925	766 ± 67	810 ± 71	896 ± 45	978 ± 131
214606_at TSPAN-2	tetraspan 2	0.0427	-0.1270	0.0584	0.2183	0.0692	20 ± 5	30 ± 9	26 ± 4	46 ± 9
213969_at TSPAN-5	tetraspan 5	0.0358	-0.0168	0.0430	-0.0235	0.0331	82 ± 12	115 ± 12	110 ± 25	187 ± 40
209803_s_at TSSC3	tumor suppressing subtransferable candidate 3	0.0384	-0.0625	-0.0085	0.3506	0.0790	60 ± 11	34 ± 14	61 ± 15	92 ± 18
204772_s_at TTF1	transcription termination factor, RNA polymerase I	0.0008	-0.0039	0.2616	-0.0552	0.0162	177 ± 13	170 ± 27	212 ± 15	283 ± 41
219728_at TTID	titin immunoglobulin domain protein	0.3587	-0.0302	0.4675	-0.0786	0.1657	252 ± 42	378 ± 52	530 ± 159	515 ± 77
208195_at TTN	titin	0.0050	0.0000	0.0059	-0.0187	0.0001	124 ± 12	165 ± 19	168 ± 18	286 ± 32
211460_at TTTY9	testis-specific transcript, Y-linked 9	0.0383	-0.1631	0.0287	-0.4758	0.1257	133 ± 11	195 ± 45	155 ± 12	232 ± 44
209074_s_at TUBA	TUBA protein	0.0001	-0.0002	0.1100	-0.0901	0.0016	11683 ± 777 2319 ± 1038	16105 ± 756 6779 ± 16986		
210527_x_at TUBA2	tubulin, α 2	0.1207	-0.0184	0.2401	-0.3468	0.0671	455 ± 34	496 ± 25	506 ± 50	603 ± 34
209118_s_at TUBA3	tubulin, α 3	0.0225	-0.0270	0.4465	-0.1753	0.0798	17518 ± 697 5982 ± 1634	1214 ± 1907 0551 ± 1861		
220069_at TUBA8	tubulin, α 8	0.1944	-0.0196	0.3686	-0.1901	0.0958	66 ± 6	78 ± 13	92 ± 10	115 ± 22
205854_at TULP3	tubby like protein 3	0.0010	-0.0300	0.4674	-0.4840	0.1208	470 ± 66	481 ± 75	591 ± 55	746 ± 141
201009_s_at TXNIP	thioredoxin interacting protein	0.0020	-0.0559	0.0682	-0.1020	0.0793	1333 ± 152	1840 ± 221	2148 ± 152	2017 ± 364
205546_s_at TYK2	tyrosine kinase 2	0.0372	-0.0565	-0.3490	-0.0534	0.0864	365 ± 50	505 ± 57	564 ± 68	538 ± 49
205300_s_at U1SNRNP8P	U1-snRNP binding protein homolog	0.0067	-0.1553	-0.2911	0.2136	0.2862	213 ± 18	198 ± 25	243 ± 20	292 ± 62
213876_x_at U2AF1RS2	U2 sn. nuclear ribonucleoproteol. aux. factor sm. subunit 2	0.0029	-0.0028	0.4005	0.1366	0.0117	1007 ± 68	962 ± 126	1230 ± 122	1782 ± 300
218381_s_at U2AF65	U2 small nuclear ribonucleoprotein auxiliary factor	0.1736	-0.0317	-0.0046	-0.3796	0.0079	756 ± 37	635 ± 29	875 ± 51	831 ± 54
219192_at UBAP2	ubiquitin associated protein 2	0.0005	-0.0506	0.0809	-0.2586	0.1268	778 ± 51	931 ± 110	1125 ± 95	1197 ± 231
202954_at UBE2C	ubiquitin-conjugating enzyme E2C	0.0761	-0.0146	0.1097	-0.1087	0.0333	385 ± 21	417 ± 28	408 ± 21	551 ± 70
200676_s_at UBE2L3	ubiquitin-conjugating enzyme E2L 3	0.0230	-0.3251	-0.2583	-0.3165	0.1420	1172 ± 97	1166 ± 64	1557 ± 153	1275 ± 190
213822_s_at UBE3B	ubiquitin protein ligase	0.0439	-0.0003	-0.4631	-0.1843	0.0020	184 ± 12	213 ± 40	223 ± 25	345 ± 18
209088_s_at UBN1	ubiquitin 1	0.0234	-0.0052	0.1980	-0.0516	0.0131	392 ± 42	406 ± 39	461 ± 29	704 ± 128
205687_at UBPH	similar to ubiquitin binding protein	0.0255	-0.0580	-0.4609	0.1409	0.0353	223 ± 10	235 ± 20	222 ± 21	319 ± 44
206072_at UCN	urocortin	0.0379	-0.0042	-0.4247	-0.4671	0.0782	124 ± 17	112 ± 19	161 ± 22	215 ± 45
204881_s_at UGCG	UDP-glucose ceramide glucosyltransferase	0.1100	-0.0123	-0.0983	-0.2782	0.0477	544 ± 27	558 ± 37	625 ± 39	667 ± 27
221304_at UGT1A	UDP glucosyltransferase 1 family, polypeptide A cluster	0.2831	-0.0213	0.0476	-0.1752	0.0113	74 ± 9	88 ± 8	68 ± 7	123 ± 18
206094_x_at UGT1A6	UDP glucosyltransferase 1 family, polypeptide A6	0.0845	-0.0153	0.0327	-0.4902	0.0146	200 ± 12	237 ± 37	228 ± 29	336 ± 33
212144_at UNC84B	unc-84 homolog B	0.0249	-0.0083	-0.1889	-0.0949	0.1144	1657 ± 188	1813 ± 174	2261 ± 306	2366 ± 242
202330_s_at UNG	uracil-DNA glycosylase	0.0164	-0.0148	-0.2500	-0.0828	0.0352	417 ± 36	427 ± 11	531 ± 35	522 ± 37
214323_s_at UPF3A	similar to yeast Upf3, variant A	0.6766	-0.0295	0.4306	-0.0881	0.3369	1877 ± 56	2054 ± 221	2182 ± 204	2313 ± 169
222236_s_at UPLC1	up-regulated in liver cancer 1	0.0029	-0.0212	-0.2315	-0.2488	0.1559	449 ± 63	494 ± 33	528 ± 29	634 ± 81
208971_at UROD	uroporphyrinogen decarboxylase	0.0146	-0.2858	0.0884	-0.0153	0.3630	373 ± 26	416 ± 32	464 ± 23	441 ± 68
202152_x_at USF2	upstream transcription factor 2, c-fos interacting	0.1494	-0.0250	0.1606	0.3764	0.1205	1178 ± 107	1321 ± 162	1321 ± 79	1682 ± 226

Web Table 5 (38)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
202413_s_at	USP1	ubiquitin specific protease 1	0.0362	-0.0028	0.2163	-0.0304	0.0367	615 ± 25	700 ± 60	818 ± 56	802 ± 66
205358_at	USP13	ubiquitin specific protease 13	0.0082	-0.0799	0.1951	-0.4696	0.1907	506 ± 27	537 ± 40	544 ± 62	679 ± 92
214674_at	USP19	ubiquitin specific protease 19	0.0744	-0.0118	0.0007	-0.0251	0.0021	107 ± 7	208 ± 23	184 ± 27	229 ± 23
200083_at	USP22	ubiquitin specific protease 22	0.0168	-0.2529	0.2062	0.3971	0.2349	2573 ± 114	2652 ± 161	2909 ± 107	2933 ± 119
221654_s_at	USP3	ubiquitin specific protease 3	0.2221	-0.0010	-0.1238	0.4590	0.0088	314 ± 23	313 ± 15	328 ± 21	446 ± 48
211800_s_at	USP4	ubiquitin specific protease 4	0.3448	-0.0044	0.1192	-0.1600	0.0456	733 ± 37	777 ± 33	852 ± 25	871 ± 45
201498_at	USP7	ubiquitin specific protease 7	0.0121	-0.1105	0.4675	-0.4097	0.1883	1397 ± 77	1464 ± 82	1646 ± 121	1804 ± 234
205139_s_at	UST	uronyl-2-sulfotransferase	0.0095	-0.0170	0.2404	0.4676	0.0150	351 ± 15	337 ± 31	462 ± 39	450 ± 34
203991_s_at	UTX	ubiq. transcribed tetrapeptide repeat gene, X chrom.	0.0000	-0.0071	-0.3630	-0.4187	0.0066	226 ± 15	260 ± 35	376 ± 26	360 ± 48
203241_at	UVRAG	UV radiation resistance associated gene	0.5963	-0.0300	-0.0057	0.0995	0.0418	370 ± 12	329 ± 43	353 ± 15	430 ± 27
201336_at	VAMP3	vesicle-associated membrane protein 3	0.0120	-0.0041	0.4627	-0.3955	0.0338	2793 ± 240	3110 ± 425	3813 ± 281	4085 ± 404
208626_s_at	VAT1	vesicle amine transport protein 1 homolog	0.0328	-0.0792	-0.3879	-0.1109	0.3873	905 ± 107	1035 ± 94	1110 ± 135	1152 ± 80
203868_s_at	VCAM1	vascular cell adhesion molecule 1	0.0476	-0.0100	0.3036	-0.0610	0.0610	185 ± 32	221 ± 27	350 ± 86	358 ± 31
214843_s_at	VDU1	pVHL-interacting deubiquitinating enzyme 1	0.2428	-0.0113	0.0512	-0.1063	0.1790	472 ± 25	500 ± 35	551 ± 13	590 ± 71
203693_s_at	VEGFB	vascular endothelial growth factor B	0.1062	-0.0186	0.0747	0.4652	0.1145	332 ± 12	397 ± 43	411 ± 41	494 ± 77
205946_at	VEGFC	vascular endothelial growth factor C	0.1971	-0.0003	0.2166	-0.1999	0.0113	152 ± 19	141 ± 19	159 ± 6	238 ± 31
203255_at	VIT1	vitiligo-associated protein VIT-1	0.0054	-0.0066	-0.3252	-0.4356	0.0270	813 ± 110	629 ± 63	1033 ± 81	1192 ± 195
207671_s_at	VMD2	vitelliform macular dystrophy	0.0154	-0.2132	-0.3657	-0.3952	0.3530	258 ± 36	338 ± 64	303 ± 37	383 ± 67
203292_s_at	VPS11	vacuolar protein sorting 11	0.4016	-0.0474	0.0573	-0.3676	0.0595	886 ± 60	908 ± 68	870 ± 62	1127 ± 89
205126_at	VRK2	vacuolar protein sorting 2	0.1704	-0.0024	-0.4979	-0.1383	0.0759	439 ± 39	502 ± 44	521 ± 41	672 ± 109
221593_s_at	VRP	vacuolar related kinase 2	0.0752	-0.0372	0.1694	-0.0774	0.3441	472 ± 47	507 ± 34	523 ± 23	590 ± 66
38964_f_at	WAS	vascular Rab-GAP/TBC-containing	0.1578	-0.0080	0.0339	-0.2478	0.0261	1682 ± 175	2132 ± 324	1683 ± 153	2946 ± 505
221725_at	WASF2	Wiskott-Aldrich syndrome	0.0063	-0.0020	0.4336	-0.1712	0.0232	592 ± 67	693 ± 100	801 ± 54	949 ± 100
221247_s_at	WBSR16	WAS protein family, member 2	0.1451	-0.0280	0.2930	0.4353	0.1813	370 ± 18	416 ± 40	439 ± 20	468 ± 49
213670_x_at	WBSR208	Williams-Beuren syndrome chromosome region 16	0.0115	-0.5489	-0.0301	-0.2821	0.7051	378 ± 36	353 ± 67	445 ± 31	427 ± 104
211788_at	WBSR5	Williams-Beuren Syndrome critical region protein 20 copy B	0.0095	-0.0109	-0.3131	0.0705	0.0266	199 ± 23	167 ± 13	233 ± 27	329 ± 59
217734_s_at	WDR6	Williams-Beuren syndrome chromosome region 5	0.0018	-0.0121	-0.2191	-0.2255	0.1072	1095 ± 136	1158 ± 98	1469 ± 146	1650 ± 286
203892_at	WFDC2	WD repeat domain 6	0.1074	-0.0181	0.3771	0.2102	0.0384	229 ± 22	217 ± 27	309 ± 23	339 ± 51
202908_at	WFS1	WAP four-disulfide core domain 2	0.0297	-0.5950	-0.2990	0.4335	0.0925	1434 ± 121	1411 ± 112	1836 ± 155	1454 ± 128
34225_at	WHSC2	Wolfram syndrome 1	0.0571	-0.0013	-0.3942	-0.1258	0.0158	435 ± 26	474 ± 11	500 ± 40	594 ± 42
212050_at	WIRE	Wolf-Hirschhorn syndrome candidate 2	0.0183	-0.0502	0.0931	-0.3836	0.1597	1550 ± 84	1773 ± 172	1856 ± 129	1968 ± 157
217681_at	WNT7B	WIRE protein	0.4679	-0.0473	0.2906	-0.4688	0.0730	93 ± 15	89 ± 25	96 ± 23	172 ± 32
205567_at	WRN	wingless-type MMTV integration site family, member 7B	0.4775	-0.0413	0.2670	-0.0975	0.1858	175 ± 14	167 ± 19	213 ± 16	199 ± 17
218276_s_at	WW45	Werner syndrome	0.0011	-0.0002	0.4794	-0.3976	0.0028	309 ± 11	323 ± 28	351 ± 21	435 ± 28
219077_s_at	WWOX	WW domain containing oxidoreductase	0.4111	-0.0026	-0.0585	-0.2335	0.0539	1243 ± 109	1412 ± 189	1500 ± 106	1972 ± 296
210200_at	WWP2	Nedd4-like ubiquitin-protein ligase	0.0806	-0.0011	0.0066	-0.0105	0.0036	216 ± 15	268 ± 19	241 ± 18	354 ± 43
213900_at	X123	Friedreich ataxia region gene X123	0.0034	-0.0007	0.2036	-0.3521	0.0089	835 ± 93	1026 ± 104	1221 ± 137	1533 ± 207
200670_at	XBP1	X-box binding protein 1	0.0110	-0.1117	-0.3637	-0.4808	0.1401	465 ± 45	450 ± 46	448 ± 36	596 ± 66
202933_s_at	YES1	y-jes-1 Yamaguchi sarcoma viral oncogene homolog 1	0.0385	-0.0042	0.0391	-0.0003	0.0156	609 ± 56	847 ± 86	991 ± 125	942 ± 67
200047_s_at	YY1	YY1 transcription factor	0.1469	-0.0372	-0.4687	-0.2020	0.3365	1668 ± 53	1596 ± 103	1823 ± 108	1861 ± 181
213051_at	ZAP	likely ortholog of rat zinc-finger antiviral protein	0.0498	-0.0005	-0.3714	-0.4265	0.0400	714 ± 80	722 ± 88	877 ± 39	1137 ± 187
219266_at	ZBRK1	zinc-finger protein ZBRK1	0.0089	-0.1478	0.0012	-0.1152	0.0170	100 ± 8	155 ± 18	131 ± 10	158 ± 16

Web Table 5 (39)

Probe set Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
221646_s_at	zinc finger, DHHC domain containing 11	0.0096	-0.0202	-0.2738	-0.1884	0.0245	835 ± 178	873 ± 97	1677 ± 285	1364 ± 242
219779_at	zinc finger homeodomain 4	0.0272	-0.1113	0.1320	-0.1867	0.4714	684 ± 81	695 ± 71	796 ± 52	880 ± 160
213130_at	zinc finger protein ZFP100	0.0123	-0.0033	-0.2703	-0.4641	0.0442	153 ± 18	172 ± 19	210 ± 19	256 ± 42
201531_at	zinc finger protein 36, C3H type, homolog	0.6731	-0.0278	-0.0342	-0.3656	0.3619	803 ± 167	737 ± 212	999 ± 204	1300 ± 334
201369_s_at	zinc finger protein 36, C3H type, homolog	0.0119	0.0000	0.1361	-0.0031	0.0011	177 ± 26	227 ± 23	238 ± 22	408 ± 66
214310_s_at	zinc finger protein-like 1	0.0041	-0.0657	-0.3436	-0.2014	0.1842	105 ± 14	108 ± 15	118 ± 8	164 ± 36
206373_at	Zic family member 1	0.0963	-0.0008	0.2570	-0.1077	0.0193	687 ± 91	1023 ± 124	1439 ± 202	1568 ± 335
221842_s_at	zinc finger protein 131	0.0011	-0.0492	0.4043	-0.4449	0.0060	505 ± 42	574 ± 95	837 ± 65	677 ± 58
37254_at	zinc finger protein 133	0.0157	-0.0360	-0.2098	0.1119	0.0962	404 ± 13	387 ± 26	445 ± 31	500 ± 51
206240_s_at	zinc finger protein 136	0.0039	0.0000	0.0098	-0.0071	0.0001	248 ± 13	321 ± 14	323 ± 30	480 ± 48
207394_at	zinc finger protein 137	0.2121	-0.0119	0.3015	-0.1603	0.2581	191 ± 18	197 ± 14	210 ± 20	243 ± 21
205883_at	zinc finger protein 145	0.0001	-0.0142	-0.1180	0.1035	0.0247	1629 ± 100	1486 ± 174	2137 ± 318	2501 ± 292
203318_s_at	zinc finger protein 148	0.0199	-0.1740	0.0544	-0.2266	0.2069	910 ± 96	1146 ± 153	1250 ± 113	1332 ± 229
203602_s_at	zinc finger protein 151	0.0937	-0.0387	-0.2431	0.1093	0.0618	381 ± 23	372 ± 28	354 ± 24	504 ± 74
202173_s_at	zinc finger protein 161	0.0762	-0.0023	0.3347	-0.0528	0.0296	479 ± 56	618 ± 84	770 ± 84	799 ± 103
205497_at	zinc finger protein 175	0.0370	-0.4099	0.4828	0.4024	0.4257	310 ± 28	335 ± 39	386 ± 15	341 ± 44
219495_s_at	zinc finger protein 180	0.9872	-0.0376	0.0582	-0.1923	0.3723	177 ± 14	184 ± 23	182 ± 12	228 ± 36
204234_s_at	zinc finger protein 195	0.0390	-0.4104	-0.1744	0.4659	0.5731	298 ± 20	318 ± 24	361 ± 19	356 ± 73
202778_s_at	zinc finger protein 198	0.0119	-0.0137	0.2370	-0.0016	0.0046	929 ± 42	961 ± 43	1140 ± 37	1030 ± 41
204327_s_at	zinc finger protein 202	0.0068	-0.0290	-0.4696	0.4615	0.1103	285 ± 15	322 ± 33	329 ± 27	403 ± 51
205437_at	zinc finger protein 211	0.0657	-0.0412	0.4292	-0.4840	0.2890	324 ± 17	349 ± 17	365 ± 29	417 ± 60
202423_at	zinc finger protein 220	0.0064	-0.0099	-0.2274	-0.3115	0.1206	1533 ± 121	1603 ± 87	1884 ± 160	1925 ± 160
219123_at	zinc finger protein 232	0.0264	-0.0696	0.2808	-0.3583	0.0920	322 ± 25	395 ± 54	357 ± 23	479 ± 69
47571_at	zinc finger protein 236	0.1353	-0.0078	0.4862	0.4037	0.0314	373 ± 26	362 ± 8	374 ± 13	504 ± 64
215948_x_at	zinc finger protein 237	0.0393	-0.0042	0.3199	-0.0229	0.0185	90 ± 8	101 ± 14	144 ± 9	133 ± 18
203247_s_at	zinc finger protein 24	0.0036	-0.0204	0.4647	-0.0326	0.1285	808 ± 84	951 ± 65	988 ± 90	1108 ± 105
208900_x_at	zinc finger protein 253	0.0950	-0.0367	0.0014	-0.0328	0.0342	203 ± 10	310 ± 33	283 ± 33	308 ± 30
208862_at	zinc finger protein 254	0.0076	-0.2379	0.1219	-0.0074	0.3517	60 ± 7	78 ± 10	76 ± 4	103 ± 35
205917_at	zinc finger protein 264	0.0017	-0.0477	0.0676	-0.2724	0.0476	490 ± 25	610 ± 59	647 ± 44	711 ± 80
209989_at	zinc finger protein 268	0.0017	-0.0202	0.0242	0.2564	0.0568	131 ± 11	165 ± 44	211 ± 20	238 ± 32
204937_s_at	zinc finger protein 274	0.3553	-0.0262	-0.2940	-0.3504	0.1133	646 ± 41	660 ± 51	622 ± 44	782 ± 52
215887_at	zinc finger protein 277	0.0149	-0.0202	-0.0578	0.4757	0.1088	300 ± 24	275 ± 24	330 ± 19	424 ± 63
209494_s_at	zinc finger protein 278	0.0042	-0.0001	0.2082	0.4022	0.0012	341 ± 21	358 ± 28	408 ± 26	465 ± 64
205383_s_at	zinc finger protein 288	0.0399	-0.7879	0.0396	-0.4225	0.8304	2784 ± 275	2856 ± 331	3603 ± 335	4851 ± 478
211975_at	zinc finger protein 289, ID1 regulated	0.6879	-0.0458	-0.2701	-0.0232	0.4415	1223 ± 88	1336 ± 130	1362 ± 117	1331 ± 150
209538_at	zinc finger protein 32	0.0273	-0.1559	-0.2914	0.2961	0.3364	418 ± 23	462 ± 85	507 ± 34	548 ± 89
37860_at	zinc finger protein 337	0.0004	-0.0158	0.3941	0.4081	0.0189	563 ± 60	527 ± 65	632 ± 63	688 ± 69
219379_x_at	zinc finger protein 358	0.0436	-0.0790	-0.2317	-0.3400	0.3980	599 ± 27	678 ± 106	792 ± 62	1086 ± 185
206135_at	zinc finger protein 387	0.0578	-0.0342	-0.1281	0.0257	0.0091	1062 ± 174	1094 ± 214	1379 ± 171	1416 ± 176
40569_at	zinc finger protein 42	0.2268	-0.0016	0.1529	-0.0241	0.0354	1031 ± 75	785 ± 51	982 ± 61	1469 ± 230
206895_x_at	zinc finger protein 43	0.1458	-0.0103	-0.4816	-0.0204	0.0576	228 ± 15	264 ± 17	272 ± 17	310 ± 24
205089_at	zinc finger protein 7						174 ± 11	185 ± 12	191 ± 11	226 ± 18

Web Table 5 (40)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
221645_s_at	zinc finger protein 83	0.6657	-0.0478	0.1521	-0.0133	0.1220	283 ± 27	394 ± 44	432 ± 51	388 ± 54
204453_at	zinc finger protein 84	0.0001	-0.0192	0.2051	-0.0099	0.0592	87 ± 10	96 ± 13	133 ± 19	138 ± 21
208472_at	zinc finger protein, subfamily 1A, 4	0.0335	-0.1455	0.0288	-0.0211	0.3678	102 ± 11	138 ± 26	121 ± 12	149 ± 31
218548_x_at	putative secreted protein ZSIG11	0.1565	-0.0164	0.0785	-0.0459	0.1738	177 ± 23	203 ± 17	207 ± 14	239 ± 20
Downregulated										
203894_at	sepin 6	-0.0004	0.0000	0.4031	0.3653	0.0000	1044 ± 50	819 ± 38	788 ± 45	630 ± 20
200902_at	15 kDa selenoprotein	-0.0197	0.1069	-0.3704	-0.2702	0.2214	983 ± 59	980 ± 133	908 ± 119	712 ± 43
213666_at	phosphopantetheinyl transferase	-0.0230	0.0374	-0.4156	-0.3670	0.0001	886 ± 50	881 ± 73	635 ± 68	467 ± 42
202169_s_at	ATP-binding cassette, sub-family B, member 1	-0.0065	0.0039	0.2772	0.3595	0.1701	3196 ± 304	2882 ± 381	2542 ± 245	2128 ± 149
203196_at	ATP-binding cassette, sub-family C, member 4	-0.0395	-0.9594	0.1817	-0.0025	0.7244	189 ± 19	208 ± 25	176 ± 23	168 ± 33
209993_at	ATP-binding cassette, sub-family E, member 1	-0.0352	0.0005	0.0166	0.4480	0.0346	323 ± 17	306 ± 16	259 ± 18	217 ± 44
201873_s_at	acyl-Coenzyme A dehydrogenase family, member 8	-0.0048	0.0115	-0.0127	0.1005	0.0000	516 ± 33	619 ± 27	557 ± 20	367 ± 19
221669_s_at	acyl-Coenzyme A acetyltransferase 1	-0.0041	0.0074	0.2274	-0.3825	0.0036	518 ± 21	404 ± 30	387 ± 28	376 ± 30
206690_at	amilonide-sensitive cation channel 1, neuronal	-0.4668	0.0239	-0.2025	-0.4684	0.1186	608 ± 62	484 ± 114	558 ± 135	269 ± 81
205378_s_at	acetylcholinesterase	-0.3873	0.0453	0.4731	0.3744	0.2221	179 ± 20	163 ± 33	160 ± 25	104 ± 25
205412_at	aconitase 2, mitochondrial	-0.0004	0.0034	-0.1477	0.2538	0.0143	1199 ± 62	1204 ± 102	917 ± 106	852 ± 51
200783_s_at	acid phosphatase 1, soluble	-0.0023	0.0009	0.3895	0.4085	0.0008	3157 ± 201	2668 ± 344	1879 ± 142	2027 ± 185
217827_s_at	acid cluster protein 33	-0.0455	0.2177	-0.1581	0.0626	0.3864	1323 ± 71	1294 ± 50	1128 ± 74	1186 ± 144
206013_s_at	actin-like 6	-0.0778	0.0372	-0.3814	0.4915	0.2907	205 ± 43	194 ± 62	119 ± 29	103 ± 44
208637_x_at	actinin, α 1	-0.2078	0.0309	-0.1291	0.0461	0.0406	903 ± 46	722 ± 42	770 ± 44	720 ± 63
200720_s_at	ARP1 actin-related protein 1 homolog A, centractin α	-0.0866	0.0210	0.4297	0.2111	0.0647	573 ± 62	592 ± 47	581 ± 24	413 ± 24
202136_s_at	ARP1 actin-related protein 1 homolog B, centractin β	-0.0104	0.4508	-0.0249	0.2736	0.6529	967 ± 60	860 ± 83	886 ± 62	868 ± 73
200729_s_at	ARP2 actin-related protein 2 homolog	-0.0195	0.0277	-0.4331	-0.1967	0.0019	881 ± 64	852 ± 132	641 ± 78	376 ± 56
200996_at	ARP3 actin-related protein 3 homolog	-0.0455	0.2131	-0.3638	-0.2805	0.3749	1348 ± 130	1232 ± 245	941 ± 88	1004 ± 259
208833_s_at	acylphosphatase 2, muscle type	-0.0180	0.1385	-0.1283	0.4894	0.0966	971 ± 52	869 ± 47	769 ± 76	806 ± 48
200728_at	glycosyltransferase AD-017	-0.0005	0.0137	0.3870	-0.1555	0.0807	1130 ± 100	1120 ± 245	892 ± 52	651 ± 46
218147_s_at	TRAF and TNF receptor-associated protein	-0.0327	0.0063	0.3830	0.3037	0.0131	282 ± 21	295 ± 27	224 ± 17	194 ± 21
206046_at	a disintegrin and metalloproteinase domain 23	-0.2007	0.0081	0.2818	0.2990	0.0266	501 ± 35	473 ± 51	350 ± 21	369 ± 53
204497_at	adenylate cyclase 9	-0.0439	0.0849	0.4070	0.2887	0.3834	884 ± 86	795 ± 76	697 ± 46	699 ± 137
205746_s_at	alcohol dehydrogenase 5, cxi polypeptide	-0.0138	0.0227	-0.4412	-0.3215	0.0264	139 ± 14	184 ± 20	127 ± 18	96 ± 21
204120_s_at	adenosine kinase	-0.0269	0.2225	-0.2766	-0.3496	0.3324	160 ± 15	151 ± 8	168 ± 18	124 ± 23
208848_at	adenosine A2b receptor	-0.0002	0.0182	-0.4369	0.1306	0.0743	1093 ± 93	1035 ± 124	820 ± 88	759 ± 94
208644_at	ADP-ribosyltransferase (polymerase)	-0.0020	0.1298	-0.0196	-0.4561	0.1858	1196 ± 67	1111 ± 70	1092 ± 77	970 ± 60
217729_s_at	amino-terminal enhancer of split	-0.0963	0.0182	-0.3097	0.2767	0.0310	1037 ± 85	944 ± 63	1011 ± 82	722 ± 58
205891_at	ALL1-fused gene from chromosome 1q	-0.0083	0.0066	-0.2831	0.4497	0.0179	423 ± 11	396 ± 42	288 ± 20	305 ± 49
211071_s_at	adenylate kinase 5	-0.0076	0.0058	-0.2779	0.3669	0.0888	8001 ± 717	7003 ± 903	5924 ± 594	5054 ± 1146
219308_s_at	A kinase anchor protein 11	-0.0069	0.0166	-0.3194	0.3453	0.0220	6484 ± 741	4905 ± 604	4274 ± 512	3541 ± 708
203156_at	A kinase anchor protein 12	-0.0012	0.0001	0.2438	0.0977	0.0794	3946 ± 346	3433 ± 587	2904 ± 249	2523 ± 392
202759_s_at	A kinase anchor protein 2	-0.0251	0.0691	-0.0136	-0.3125	0.2230	1219 ± 79	1193 ± 83	1141 ± 118	928 ± 129
201425_at	aldehyde dehydrogenase 2 family	-0.0615	0.0161	-0.0228	0.0997	0.0039	6579 ± 227	5151 ± 261	5117 ± 384	4890 ± 401

Web Table 5 (41)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
203608_at	aldehyde dehydrogenase 5 family, member A1	-0.0816	0.0336	-0.3654	0.1285	0.1291	1539 ± 160	1230 ± 124	1319 ± 141	1025 ± 162
210517_s_at	aldolase C, fructose-bisphosphate	-0.0186	0.0063	0.0603	-0.3574	0.0003	1105 ± 80	1081 ± 61	989 ± 100	596 ± 48
202022_at	ALEX1 protein	-0.0254	0.0221	-0.3021	-0.2986	0.0162	9235 ± 722	1254 ± 1578	1118 ± 1163	5884 ± 187
204174_at	arachidonate 5-lipoxygenase-activating protein	-0.0089	0.5289	-0.0056	0.3400	0.2616	771 ± 118	622 ± 75	475 ± 73	661 ± 44
218694_at	autocrine motility factor receptor	-0.0168	0.0163	-0.3278	0.4239	0.0691	1010 ± 96	941 ± 101	740 ± 60	701 ± 113
202811_at	associated molecule with the SH3 domain of STAM	-0.0444	0.9850	0.3239	0.1350	0.8043	892 ± 36	871 ± 37	789 ± 57	876 ± 96
208498_s_at	amylase, α 1A; salivary	-0.0232	0.0582	-0.4185	-0.3594	0.2628	319 ± 32	348 ± 27	284 ± 23	262 ± 39
204727_at	AND-1 protein	-0.1046	0.0354	-0.1270	0.0735	0.2635	56 ± 8	42 ± 6	46 ± 11	37 ± 5
209442_x_at	ankyrin 3, node of Ranvier	-0.0507	0.0314	0.0408	0.2900	0.0931	1076 ± 39	1167 ± 82	1011 ± 55	939 ± 60
209860_s_at	annexin A7	-0.0265	0.1204	-0.3583	-0.1762	0.2317	1257 ± 99	1232 ± 145	1024 ± 58	1010 ± 109
202203_s_at	adaptor-related protein complex 2, β 1 subunit	-0.0407	0.0203	-0.0615	0.1140	0.0561	727 ± 104	657 ± 169	466 ± 91	300 ± 78
200813_at	adaptor-related protein complex 2, mu 1 subunit	-0.1009	0.0229	-0.4039	-0.1683	0.0251	2336 ± 116	2446 ± 364	2352 ± 185	1423 ± 209
208074_s_at	adaptor-related protein complex 2, sigma 1 subunit	-0.0822	0.0310	-0.2196	0.4482	0.2109	1045 ± 91	992 ± 164	929 ± 37	724 ± 118
205878_at	adaptor-related protein complex 3, β 2 subunit	-0.0587	0.0056	0.3870	0.1584	0.0674	1011 ± 132	778 ± 40	727 ± 87	639 ± 87
200615_s_at	adaptor-related protein complex 3, sigma 1 subunit	-0.0012	0.0001	-0.4392	0.0096	0.0413	916 ± 42	763 ± 87	716 ± 49	677 ± 71
210277_at	adaptor-related protein complex 4, sigma 1 subunit	-0.0204	0.1534	-0.1719	-0.3086	0.2052	126 ± 12	100 ± 17	110 ± 13	82 ± 17
202442_at	ATP binding protein associated with cell differentiation	-0.0078	0.0026	0.4166	0.3811	0.0011	4853 ± 235	4193 ± 84	3928 ± 179	3611 ± 226
211758_x_at	amyloid β precursor protein-binding, family A, member 2	-0.0271	0.0094	-0.3485	0.1203	0.0110	945 ± 98	781 ± 108	660 ± 60	513 ± 38
209871_s_at	adenomatosis polyposis coli	-0.0111	0.0003	-0.1928	0.0461	0.0308	4088 ± 350	3329 ± 423	2735 ± 284	2915 ± 277
203527_s_at	APEX nuclease	-0.0070	0.0077	-0.4214	-0.3631	0.0021	637 ± 20	511 ± 73	472 ± 57	241 ± 95
210027_s_at	heat shock protein	-0.0207	0.0185	-0.2345	0.4053	0.0246	1413 ± 86	1505 ± 114	1246 ± 79	1100 ± 53
205543_at	amyloid β precursor-like protein 2	-0.0062	0.0126	-0.0603	0.3192	0.0155	285 ± 25	223 ± 27	207 ± 21	164 ± 19
202268_s_at	amyloid β precursor protein binding protein 1, 59kDa	-0.0159	0.5330	-0.1010	-0.4897	0.6402	937 ± 46	840 ± 69	875 ± 58	816 ± 113
201176_s_at	archain 1	-0.0338	0.0587	-0.0229	-0.4217	0.1365	1095 ± 51	1044 ± 110	948 ± 44	814 ± 130
208248_x_at	ADP-ribosylation factor 1	-0.0075	0.0020	-0.0526	0.0889	0.0111	5472 ± 321	5486 ± 288	5755 ± 212	4263 ± 377
200734_s_at	ADP-ribosylation factor 3	-0.0030	0.0003	-0.3908	0.0486	0.0072	6169 ± 535	5151 ± 427	4503 ± 419	3636 ± 524
201097_s_at	ADP-ribosylation factor 4	-0.0249	0.0967	0.4321	-0.3210	0.1529	2597 ± 175	2907 ± 90	2232 ± 76	2277 ± 361
201526_at	ADP-ribosylation factor 5	-0.1202	0.0013	0.3219	0.2452	0.0238	1067 ± 97	1088 ± 100	965 ± 92	675 ± 90
200011_s_at	ADP-ribosylation factor guanine nucleotide-exchange factor 2	-0.0040	0.0032	-0.3809	0.4246	0.2742	4470 ± 387	4035 ± 478	3904 ± 387	3305 ± 405
218098_at	Arg/Abi-interacting protein ArgBP2	-0.0464	0.0005	-0.3888	0.3052	0.0224	1113 ± 71	1204 ± 65	991 ± 77	808 ± 108
204288_s_at	Rho guanine nucleotide exchange factor 3	-0.0372	0.0460	0.4211	0.2355	0.0037	666 ± 64	588 ± 45	607 ± 72	330 ± 41
211891_s_at	Rho guanine nucleotide exchange factor 4	-0.2452	0.0486	0.3604	0.0476	0.5472	461 ± 58	421 ± 40	406 ± 45	364 ± 33
218501_at	Cdc42 guanine nucleotide exchange factor 9	-0.0087	0.0047	-0.2544	0.0844	0.1657	1997 ± 266	1700 ± 177	1353 ± 184	1370 ± 275
215506_s_at	ras homolog gene family, member 1	-0.0710	0.0287	-0.0997	0.4589	0.1225	154 ± 18	132 ± 8	115 ± 21	102 ± 10
201228_s_at	ariadne homolog 2	-0.0154	0.1633	0.1764	-0.3651	0.0896	166 ± 13	196 ± 23	135 ± 8	144 ± 20
203264_s_at	ADP-ribosylation factor-like 1	-0.0080	0.0398	-0.0682	0.1120	0.0903	2514 ± 265	2053 ± 361	1782 ± 211	1483 ± 325
201659_s_at	ADP-ribosylation factor-like 7	-0.0294	0.0387	-0.2117	0.2681	0.0280	361 ± 21	309 ± 31	251 ± 19	278 ± 31
202206_at	aryl-hydrocarbon receptor nuclear translocator 2	-0.0232	0.0060	0.4689	0.2053	0.0985	451 ± 60	365 ± 53	291 ± 41	305 ± 33
218868_at	actin-related protein 3-β	-0.1288	0.0209	0.3049	0.1522	0.0718	782 ± 141	520 ± 69	466 ± 47	452 ± 80

Web Table 5 (42)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
200950_at	ARPC1A	actin related protein 23 complex, subunit 1A, 41kDa	-0.0223	0.0982	0.4727	0.2339	0.3586	1375 ± 147	1270 ± 182	992 ± 69	1047 ± 279
202886_at	ARPC2	actin related protein 23 complex, subunit 2, 34kDa	-0.0216	0.0180	0.1596	-0.4914	0.0023	2960 ± 138	2340 ± 220	2708 ± 198	1963 ± 93
213513_x_at	ARPC3	actin related protein 23 complex, subunit 3, 21kDa	-0.0425	0.0321	0.3714	-0.2868	0.0922	3327 ± 350	3014 ± 187	2846 ± 138	2398 ± 213
211963_s_at	ARPC5	actin related protein 23 complex, subunit 5, 16kDa	-0.0202	0.0260	0.1618	0.2179	0.7378	1601 ± 65	1695 ± 82	1526 ± 141	1562 ± 29
221482_s_at	ARPP-19	cyclic AMP phosphoprotein, 19 kD	-0.0612	0.0090	-0.4479	0.4854	0.0512	2398 ± 315	2248 ± 244	2087 ± 163	1459 ± 10
217776_at	ARSDR1	androgen-regulated short-chain dehydrogenase/reductase 1	-0.0167	0.0941	0.4113	-0.4799	0.3016	1893 ± 177	1817 ± 207	1558 ± 136	1426 ± 256
208738_at	AS3	androgen-induced prostate proliferative shut-off assoc. protein	-0.0400	0.0210	-0.4489	0.4450	0.1092	1115 ± 100	1082 ± 137	920 ± 73	760 ± 224
213902_at	ASAH1	N-acylsphingosine amidohydrolase 1	-0.0909	0.0061	0.2001	0.1464	0.0434	1133 ± 135	919 ± 40	818 ± 73	703 ± 220
208517_s_at	ASH2L	ash2-like	-0.0056	0.0721	0.3679	0.4077	0.0913	1287 ± 88	1330 ± 58	1041 ± 96	114 ± 91
204742_s_at	ASMTL	acetylserotonin O-methyltransferase-like	-0.0354	0.0134	0.3775	-0.3333	0.1775	694 ± 91	643 ± 112	531 ± 48	444 ± 74
202024_at	ASNA1	arsA arsenite transporter, ATP-binding, homolog 1	-0.0422	0.0578	-0.2595	-0.1976	0.1275	638 ± 64	674 ± 83	628 ± 45	445 ± 87
36554_at	ASPH	aspartate β-hydroxylase	-0.0021	0.0017	-0.0265	0.2221	0.0458	275 ± 22	276 ± 36	249 ± 25	172 ± 11
210895_s_at	ASTN	astrotactin	-0.0027	0.0014	-0.3201	0.3528	0.0005	561 ± 45	350 ± 40	374 ± 51	246 ± 20
208758_at	ATIC	IMP cyclohydrolase	-0.0177	0.2268	-0.0028	0.1027	0.0220	1080 ± 27	987 ± 65	748 ± 99	980 ± 87
203285_s_at	ATP1A2	ATPase, Na ⁺ /K ⁺ transporting, α 2 polypeptide	-0.4108	0.0472	0.0293	-0.0678	0.0707	3247 ± 179	3350 ± 295	3451 ± 224	2494 ± 174
201243_s_at	ATP1B1	ATPase, Na ⁺ /K ⁺ transporting, β 1 polypeptide	-0.0223	0.2349	-0.2176	-0.2624	0.4412	10569 ± 551	9872 ± 1011	10155 ± 496	8878 ± 930
213197_at	ATP2A2	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	-0.0197	0.0488	-0.0069	0.1614	0.0133	1692 ± 157	1448 ± 203	1238 ± 168	888 ± 118
209186_at	ATP2B1	ATPase, Ca ⁺⁺ transporting, plasma membrane 1	-0.0086	0.0040	0.3046	0.4770	0.0508	3230 ± 62	2685 ± 287	2553 ± 162	2404 ± 294
215716_s_at	ATP2B2	ATPase, Ca ⁺⁺ transporting, plasma membrane 2	-0.0241	0.0005	0.2534	0.2047	0.0342	1788 ± 270	1625 ± 233	1154 ± 91	893 ± 232
211137_s_at	ATP2C1	ATPase, Ca ⁺⁺ transporting, type 2C, member 1	-0.0439	0.0059	0.0287	-0.1215	0.2042	655 ± 48	733 ± 41	629 ± 32	576 ± 69
204685_s_at	ATP5A1	ATP synthase, F1 complex, α subunit	-0.0068	0.0022	-0.3724	0.4763	0.0151	2397 ± 264	2403 ± 254	2013 ± 304	1201 ± 48
213738_s_at	ATP5B	ATP synthase, F1 complex, γ polypeptide	-0.0038	0.0276	-0.2752	0.3967	0.0135	4827 ± 452	4315 ± 520	3405 ± 479	2586 ± 329
213366_x_at	ATP5C1	ATP synthase, F1 complex, γ polypeptide 1	-0.0009	0.0018	-0.3409	0.2362	0.0109	3990 ± 407	3464 ± 431	2580 ± 224	2253 ± 431
208870_x_at	ATP5E	ATP synthase, F1 complex, epsilon	-0.0235	0.0145	0.2506	-0.2572	0.0284	4060 ± 484	3868 ± 438	2572 ± 192	2741 ± 450
217801_at	ATP5F1	ATP synthase, F0 complex, subunit b, isoform 1	-0.0084	0.0391	-0.4077	0.1998	0.0327	5191 ± 250	4834 ± 452	4800 ± 274	3806 ± 307
211755_s_at	ATP5G3	ATP synthase, F0 complex, subunit c, isoform 3	-0.0175	0.0355	0.1719	-0.4570	0.0996	3548 ± 347	2974 ± 389	2407 ± 251	2435 ± 482
207508_at	ATP5H	ATP synthase, F0 complex, subunit d	-0.0133	0.0201	-0.4996	0.2836	0.0730	2559 ± 328	2249 ± 262	1626 ± 211	1695 ± 306
210149_s_at	ATP5J	ATP synthase, F0 complex, subunit F6	-0.0097	0.0254	-0.1686	0.2712	0.0551	4108 ± 577	3508 ± 548	2431 ± 258	2522 ± 487
202325_s_at	ATP5J2	ATP synthase, F0 complex, subunit f, isoform 2	-0.0131	0.0098	-0.2612	0.3466	0.0874	2953 ± 210	2575 ± 296	2501 ± 93	1970 ± 389
208745_at	ATP5L	ATP synthase, F0 complex, subunit g	-0.0183	0.0054	-0.2001	0.3686	0.0379	1204 ± 87	1193 ± 157	903 ± 128	743 ± 132
207573_x_at	ATP5O	ATP synthase, F1 complex, O subunit	-0.0049	0.0097	-0.3982	0.3684	0.0470	1768 ± 123	1686 ± 274	1364 ± 140	1045 ± 152
207809_s_at	ATP6IP1	ATPase, lysosomal interacting protein 1	-0.0538	0.0238	-0.2033	0.0852	0.0640	2289 ± 324	1795 ± 272	1395 ± 177	1469 ± 126
200818_at	ATP6IP2	ATPase, lysosomal interacting protein 2	-0.0224	0.0239	0.4487	0.1979	0.0717	3259 ± 265	2919 ± 281	2509 ± 230	2123 ± 448
36994_at	ATP6V0C	ATPase, H ⁺ transporting, lysosomal 16kDa, V0 subunit c	-0.0333	0.1039	-0.2408	0.4923	0.2577	6835 ± 564	6391 ± 715	5204 ± 323	5395 ± 965
201971_s_at	ATP6V1A1	ATPase, lysosomal V1 subunit A, isoform 1	-0.0446	0.0933	-0.2416	-0.4302	0.1629	168 ± 38	162 ± 43	73 ± 14	113 ± 33
202872_at	ATP6V1C1	ATPase, lysosomal V1 subunit C, isoform 1	-0.1005	0.0013	-0.3820	-0.3411	0.0143	850 ± 66	858 ± 20	712 ± 43	585 ± 80
201444_s_at	ATP6V1D	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D	-0.0044	0.0026	-0.1328	0.1932	0.0732	1106 ± 231	873 ± 154	545 ± 80	556 ± 161
208899_x_at	ATP6V1E1	ATPase, lysosomal V1 subunit E isoform 1	-0.0056	0.0016	-0.4344	0.1406	0.0094	1449 ± 142	1160 ± 177	813 ± 81	920 ± 133
208678_at	ATP6V1F	ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F	-0.0392	0.0232	-0.1981	-0.2157	0.0220	3167 ± 409	2667 ± 438	2000 ± 163	1677 ± 307

Web Table 5 (43)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
201527_at	ATPase, lysosomal V1 subunit G isoform 2	-0.0079	0.0009	0.4995	0.2629	0.0629	2988 ± 209	3036 ± 347	2711 ± 260	2007 ± 314
214762_at	ATPase, lysosomal V1 subunit H	-0.0067	0.0020	-0.4839	0.2505	0.0068	3258 ± 540	2582 ± 468	1551 ± 245	1192 ± 219
219659_at	ATPase, Class I, type 8A, member 2	-0.0779	0.0336	0.4087	-0.3513	0.1941	842 ± 106	768 ± 108	641 ± 74	571 ± 73
209903_s_at	ataxia telangiectasia and Rad3 related	-0.0244	0.0957	-0.2102	0.3627	0.1287	917 ± 77	786 ± 99	700 ± 28	701 ± 68
221504_s_at	atractin	-0.0002	0.0003	-0.0948	0.1710	0.0289	2552 ± 336	2233 ± 475	1589 ± 185	1170 ± 305
208861_s_at	α thalassemia/mental retardation syndrome X-linked	-0.0206	0.1848	-0.3421	-0.1373	0.4447	3094 ± 118	2988 ± 217	2946 ± 139	2681 ± 240
205052_at	AU RNA binding protein/Venoyl-Coenzyme A hydratase	-0.0089	0.0843	-0.4071	0.3211	0.3314	858 ± 95	795 ± 72	733 ± 66	657 ± 70
202686_s_at	AXL receptor tyrosine kinase	-0.0344	0.0565	-0.1005	-0.2097	0.7703	697 ± 68	735 ± 40	685 ± 76	630 ± 75
216231_s_at	β2-microglobulin	-0.0485	0.2655	-0.1112	-0.3310	0.4688	7997 ± 1038	3813 ± 1385	3780 ± 1676	5051 ± 861
217452_s_at	UDP-Gal4GlcNAc β 1,3-galactosyltransferase, polypeptide 2	-0.1651	0.0332	-0.4916	-0.1578	0.0209	378 ± 48	395 ± 69	415 ± 39	189 ± 26
206233_at	UDP-Gal4GlcNAc β 1,4-galactosyltransferase, polypeptide 6	-0.0624	0.0076	-0.2410	0.4600	0.0452	428 ± 60	342 ± 80	347 ± 45	181 ± 42
215728_s_at	brain acyl-CoA hydrolase	-0.0326	0.3261	-0.4015	-0.3714	0.1547	223 ± 32	212 ± 38	129 ± 18	173 ± 36
212517_at	BCL2-associated athanogene 5	-0.0373	0.0235	-0.1717	0.1017	0.0024	1123 ± 41	1052 ± 69	901 ± 46	764 ± 93
202985_s_at	brain-specific angiogenesis inhibitor 2	-0.0408	0.0034	0.4526	0.0301	0.1562	1489 ± 81	1355 ± 86	1379 ± 26	1250 ± 75
204966_at	brain-specific angiogenesis inhibitor 3	-0.0156	0.0024	0.3747	0.2132	0.0029	2809 ± 219	2051 ± 120	2491 ± 244	1672 ± 49
205084_at	B-cell receptor-associated protein BAP29	-0.5328	0.0442	-0.4716	-0.3510	0.0891	148 ± 19	137 ± 20	146 ± 10	87 ± 19
213318_s_at	HLA-B associated transcript 3	-0.0874	0.0288	-0.4008	-0.2591	0.0367	1678 ± 137	1814 ± 88	1683 ± 102	1302 ± 116
211703_s_at	β-amyloid binding protein precursor	-0.0158	0.1296	-0.3977	-0.2633	0.1250	388 ± 35	440 ± 24	283 ± 47	320 ± 66
202121_s_at	putative breast adenocarcinoma marker	-0.1174	0.0225	0.2527	-0.1914	0.0719	955 ± 74	945 ± 119	871 ± 93	620 ± 55
203053_at	breast carcinoma amplified sequence 2	-0.1778	0.0458	-0.4704	0.3028	0.0751	778 ± 106	703 ± 80	461 ± 32	570 ± 100
219107_at	B-cell CLL/lymphoma 11A	-0.0120	0.0013	0.2249	0.1422	0.0932	615 ± 106	640 ± 32	457 ± 78	337 ± 96
219497_s_at	B-cell CLL/lymphoma 11B	-0.0336	0.0150	-0.3391	0.1646	0.0178	718 ± 94	570 ± 58	512 ± 95	328 ± 46
202518_at	B-cell CLL/lymphoma 7B	-0.0225	0.0406	0.2065	0.3203	0.2600	823 ± 86	795 ± 82	676 ± 83	613 ± 77
219528_s_at	bedin 1	-0.0127	0.0281	0.1457	0.4365	0.0807	1046 ± 138	786 ± 122	767 ± 119	581 ± 97
202710_at	BET1 homolog	-0.0824	0.0328	0.2249	0.0656	0.2736	661 ± 40	608 ± 32	584 ± 67	520 ± 55
208946_s_at	brain expressed, X-linked 1	-0.0084	0.0030	-0.2274	0.1509	0.0975	546 ± 40	581 ± 43	531 ± 42	415 ± 46
218332_at	basic helix-loop-helix domain containing, class B, 2	-0.0023	0.0202	-0.2446	0.2807	0.0574	7804 ± 510	7299 ± 721	5861 ± 599	5633 ± 699
201170_s_at	BBP-like protein 2	-0.0048	0.0136	-0.2592	0.4721	0.0723	2077 ± 211	2024 ± 245	1613 ± 131	1365 ± 239
203840_at	basic leucine zipper nuclear factor 1	-0.0341	0.1739	-0.4715	-0.0096	0.1845	165 ± 14	147 ± 30	131 ± 18	99 ± 21
32088_at	BCL2/adenovirus E1B 19kDa interacting protein 3	-0.0120	0.0099	0.4173	0.4551	0.0038	85 ± 9	67 ± 6	63 ± 8	40 ± 8
221478_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-0.0455	0.0866	0.3862	-0.1853	0.0537	2755 ± 131	3236 ± 153	2674 ± 284	2335 ± 126
201849_at	brain and reproductive organ-expressed	-0.0221	0.0241	0.4302	0.0848	0.0326	4048 ± 394	3440 ± 384	3065 ± 119	2666 ± 268
205550_s_at	Bernardinelli-Seip congenital lipodystrophy 2	-0.0138	0.0120	-0.3178	-0.4768	0.2589	845 ± 54	808 ± 80	697 ± 47	725 ± 60
208677_s_at	basigin	-0.0571	0.0295	-0.1860	0.3601	0.1526	789 ± 108	782 ± 105	716 ± 69	484 ± 112
208906_at	bassoon	-0.0312	0.0461	-0.2136	0.3797	0.0772	2986 ± 347	2493 ± 611	2097 ± 389	1370 ± 366
203944_x_at	butyrophilin, subfamily 2, member A1	-0.0240	0.6333	-0.1731	0.2806	0.5435	500 ± 26	489 ± 30	437 ± 19	479 ± 54
218048_at	BUP protein	-0.0261	0.1184	-0.4689	-0.2383	0.2276	861 ± 54	930 ± 72	775 ± 27	769 ± 76
204586_at	chromosome 11 open reading frame 25	-0.0234	0.0005	0.3272	0.2580	0.1293	990 ± 141	729 ± 114	708 ± 98	593 ± 113
215241_at	chromosome 12 open reading frame 5	-0.0145	0.0149	0.0598	-0.0039	0.0095	1945 ± 278	1857 ± 312	1471 ± 258	599 ± 120

Web Table 5 (44)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
219099_at C14orf2	chromosome 14 open reading frame 2	-0.0068	0.0031	-0.3120	0.1009	0.0381	234 ± 11	250 ± 15	229 ± 19	-175 ± 23
201491_at C14orf3	chromosome 14 open reading frame 3	-0.0027	0.0614	-0.0040	0.2347	0.0385	1439 ± 66	1180 ± 124	1136 ± 74	1008 ± 124
210532_s_at C1orf15	chromosome 1 open reading frame 15	-0.0109	0.0036	-0.4304	0.1401	0.0353	6081 ± 629	5182 ± 647	4197 ± 390	3708 ± 671
209755_at C1orf21	chromosome 1 open reading frame 21	-0.0208	0.0251	-0.4381	-0.4971	0.0140	1460 ± 221	1155 ± 161	741 ± 76	772 ± 136
218443_at C20orf13	chromosome 20 open reading frame 13	-0.1798	0.0281	0.3201	-0.4428	0.0706	258 ± 30	217 ± 32	172 ± 7	172 ± 25
217335_s_at C20orf44	chromosome 20 open reading frame 44	-0.1049	0.0092	0.3013	0.2834	0.0892	951 ± 90	919 ± 56	793 ± 42	717 ± 46
218359_at C20orf98	chromosome 20 open reading frame 98	-0.5784	0.0478	0.3913	0.4624	0.0705	992 ± 131	1088 ± 169	1142 ± 135	590 ± 166
206436_at C22orf1	chromosome 22 open reading frame 1	-0.2720	0.0362	0.0949	0.4410	0.1990	637 ± 43	710 ± 98	621 ± 62	489 ± 73
209418_s_at C22orf19	chromosome 22 open reading frame 19	-0.0034	0.3665	0.3584	0.0707	0.5568	252 ± 17	228 ± 8	213 ± 25	211 ± 36
221272_s_at C4orf1	chromosome 4 open reading frame 1	-0.0126	0.0054	0.2226	-0.3614	0.1142	769 ± 28	781 ± 66	731 ± 45	607 ± 57
209726_at C6orf32	chromosome 6 open reading frame 32	-0.0050	0.0017	0.2290	-0.3963	0.0230	1240 ± 143	1158 ± 144	1021 ± 92	663 ± 65
209829_at C8FW	phosphoprotein regulated by mitogenic pathways	-0.0356	0.0495	0.4126	-0.4550	0.0125	646 ± 49	639 ± 88	530 ± 57	357 ± 53
202241_at C9orf16	chromosome 9 open reading frame 16	-0.0085	0.0369	0.1424	0.0373	0.1839	552 ± 48	489 ± 38	462 ± 39	426 ± 18
222165_x_at CA11	carbonic anhydrase XI	-0.0444	0.0110	0.1698	0.3104	0.3484	1259 ± 123	1250 ± 136	1089 ± 162	914 ± 176
209726_at CABP1	calcium binding protein 1	-0.0369	0.0063	-0.3455	0.4228	0.0003	2445 ± 151	2410 ± 219	2809 ± 227	1500 ± 106
210181_s_at CACNB2	calcium channel, voltage-dependent, β 2 subunit	-0.0232	0.0251	-0.2262	0.3577	0.0435	539 ± 130	478 ± 110	274 ± 59	148 ± 28
213714_at CACNG3	calcium channel, voltage-dependent, γ subunit 3	-0.0011	0.0002	-0.3438	0.4533	0.0965	699 ± 135	447 ± 98	373 ± 75	375 ± 87
204814_at CADPS	Ca ²⁺ -dependent activator protein for secretion	-0.0307	0.0525	0.0209	-0.0307	0.0009	465 ± 16	625 ± 43	405 ± 49	419 ± 16
209563_x_at CALM1	calmodulin 1	-0.0799	0.0328	-0.3477	0.4814	0.0483	9478 ± 582	8506 ± 417	6800 ± 613	7797 ± 1024
205384_at CALM3	calmodulin 3	-0.0085	0.0008	0.0601	-0.4690	0.0009	1378 ± 179	1050 ± 144	889 ± 134	386 ± 91
212952_at CALR	calreticulin	-0.0412	0.0092	-0.3119	-0.2369	0.4102	780 ± 96	748 ± 65	676 ± 44	612 ± 68
200622_x_at CAMK1G	calcium/calmodulin-dependent protein kinase IG	-0.0071	0.0003	-0.4056	0.1882	0.0068	1472 ± 147	1607 ± 210	1149 ± 54	905 ± 93
215161_at CAMK2A	calcium/calmodulin-dependent protein kinase II α	-0.0081	0.0127	-0.2239	0.1883	0.0030	527 ± 98	367 ± 88	255 ± 65	49 ± 11
213108_at CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, β	-0.0149	0.0028	0.4553	0.0438	0.0930	5507 ± 582	4530 ± 733	4188 ± 944	2766 ± 316
212252_at CAP	adenylyl cyclase-associated protein	-0.0041	0.0200	-0.2774	0.3730	0.0569	889 ± 47	825 ± 31	778 ± 96	626 ± 56
200625_s_at CAP2	adenylyl cyclase-associated protein 2	-0.0379	0.0089	0.3239	0.2932	0.0193	3145 ± 172	2707 ± 149	2605 ± 77	2415 ± 221
212554_at CAPNS1	calpain, small subunit 1	-0.0037	0.0146	0.2367	0.4717	0.0881	3701 ± 716	2980 ± 526	2384 ± 170	1740 ± 470
215153_at CAPON	C-terminal PDZ domain ligand of neuronal nitric oxide synthase	-0.2234	0.0056	0.4427	0.0549	0.0951	793 ± 97	710 ± 115	704 ± 160	370 ± 72
200001_at CAS1	O-acetyltransferase	-0.0042	0.0058	-0.3994	0.2378	0.0954	3062 ± 173	3120 ± 252	2919 ± 222	2278 ± 340
219342_at CASP8AP2	CASP8 associated protein 2	-0.0318	0.0019	-0.1775	-0.4263	0.0552	1152 ± 130	1043 ± 129	880 ± 57	721 ± 110
222201_s_at CBARA1	calcium binding atopy-related autoantigen 1	-0.0193	0.0233	0.2591	-0.3218	0.0001	510 ± 37	483 ± 41	518 ± 21	272 ± 20
205528_s_at CBFA2T1	core-binding factor α 2, cyclin D-related	-0.3651	0.0316	0.1555	-0.2604	0.0870	189 ± 24	180 ± 8	122 ± 14	138 ± 25
216903_s_at CCK	cholecystokinin	-0.0085	0.0210	-0.1862	0.2157	0.0914	1141 ± 26	1193 ± 44	1081 ± 43	1048 ± 50
205989_at CCNA1	cyclin A1	-0.0452	0.1029	-0.2604	0.0793	0.0834	383 ± 41	296 ± 38	251 ± 20	288 ± 46
205827_at CCND2	cyclin D2	-0.0036	0.0149	0.4920	-0.2213	0.0385	2013 ± 305	1517 ± 459	815 ± 147	1078 ± 252
200953_s_at CCNG2	cyclin G2	-0.0066	0.0166	-0.3090	0.1804	0.0351	1669 ± 104	1683 ± 156	1318 ± 139	1178 ± 161
211559_s_at CCNH	cyclin H	-0.0017	0.0205	-0.2864	0.3676	0.0191	303 ± 33	247 ± 15	233 ± 24	175 ± 28
201947_s_at CCT2	chaperonin containing TCP1, subunit 2	-0.1040	0.0442	-0.1558	0.0115	0.1182	1961 ± 144	1737 ± 60	1436 ± 110	1562 ± 265
200910_at CCT3	chaperonin containing TCP1, subunit 3	-0.0068	0.1135	-0.0039	0.2583	0.1063	1682 ± 105	1396 ± 100	1491 ± 67	1288 ± 162

Web Table 5 (45)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
200877_at	CCT4	chaperonin containing TCP1, subunit 4	-0.0135	0.0565	-0.2119	0.0384	0.1370	2441 ± 400	1690 ± 221	1675 ± 194	1460 ± 323
208596_at	CCT5	chaperonin containing TCP1, subunit 5	-0.0357	0.4168	-0.0205	0.1860	0.1592	1481 ± 115	1170 ± 176	967 ± 43	1225 ± 251
204093_at	CD59	CD59 antigen p18-20	-0.0087	0.0396	-0.0258	0.2629	0.0891	977 ± 90	907 ± 144	692 ± 88	645 ± 120
200883_x_at	CDC27	cell division cycle 27	-0.0232	0.0060	-0.0030	0.1676	0.1173	1412 ± 273	1082 ± 143	1137 ± 172	663 ± 88
217881_s_at	CDC42	cell division cycle 42	-0.0092	0.0005	0.4716	0.2351	0.0080	148 ± 15	110 ± 17	120 ± 18	58 ± 11
210232_at	CDC5L	CDC5 cell division cycle 5-like	-0.0403	0.0029	0.4667	0.1006	0.0034	542 ± 63	523 ± 52	317 ± 36	321 ± 33
209056_s_at	CDH10	cadherin 10, type 2	-0.0165	0.0004	-0.3898	0.1676	0.0145	676 ± 37	624 ± 48	578 ± 26	492 ± 41
207172_s_at	CDH11	cadherin 11, type 2, OB-cadherin	-0.0038	0.0303	0.0208	-0.4522	0.0659	248 ± 23	218 ± 44	164 ± 11	153 ± 26
207173_x_at	CDH13	cadherin 13, H-cadherin	-0.0493	0.0075	-0.1495	0.1995	0.0991	892 ± 65	835 ± 64	721 ± 72	668 ± 69
206280_at	CDH18	cadherin 18, type 2	-0.2637	0.0094	0.2671	0.2251	0.1480	650 ± 70	638 ± 112	575 ± 97	385 ± 56
217574_at	CDH8	cadherin 8, type 2	-0.0110	0.7485	0.3316	-0.4476	0.2528	123 ± 11	123 ± 19	80 ± 12	121 ± 28
204726_at	CDK5	cyclin-dependent kinase 5	-0.0062	0.0005	0.3355	0.3721	0.0665	136 ± 20	107 ± 25	75 ± 19	61 ± 10
204247_s_at	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1	-0.0323	0.0150	-0.4969	-0.2199	0.0131	1026 ± 97	935 ± 76	781 ± 66	573 ± 18
204995_at	CDK7	cyclin-dependent kinase 7	-0.0163	0.0021	-0.0137	0.0265	0.1154	2690 ± 232	2480 ± 274	2387 ± 227	1808 ± 86
210240_s_at	CDKN2D	cyclin-dependent kinase inhibitor 2D	-0.0150	0.4288	-0.0701	0.3124	0.2412	298 ± 27	216 ± 31	204 ± 28	232 ± 53
211297_s_at	CDO1	cyclin-dependent kinase 1	-0.0063	0.0161	-0.2259	0.3587	0.0118	219 ± 12	186 ± 9	169 ± 32	105 ± 24
212864_at	CDS2	cysteine dioxygenase, type 2	-0.0128	0.5775	0.2281	0.0688	0.0878	830 ± 22	852 ± 27	731 ± 27	831 ± 59
204154_at	CENTG1	centaurin, γ 1	-0.0050	0.0016	0.0131	0.2700	0.0331	1251 ± 133	1046 ± 147	742 ± 76	829 ± 133
215080_s_at	CEPT1	choline/ethanolaminephosphotransferase	-0.0185	0.0128	-0.0028	-0.4291	0.0065	161 ± 25	133 ± 16	86 ± 18	58 ± 13
205651_x_at	CGEF2	cAMP-regulated guanine nucleotide exchange factor II	-0.0226	0.0565	-0.1717	-0.1712	0.0784	1436 ± 127	1375 ± 125	1386 ± 189	918 ± 47
219375_at	CGI-127	yippee protein	-0.0270	0.0252	-0.2386	0.4410	0.0060	636 ± 68	500 ± 83	568 ± 34	294 ± 31
217783_s_at	CGI-142	hepatoma-derived growth factor 2	-0.0040	0.0331	-0.2083	0.1157	0.1751	2867 ± 234	2640 ± 289	2266 ± 224	2124 ± 301
209524_at	CGI-51	CGI-51 protein	-0.0183	0.0099	0.1093	0.1474	0.0948	1729 ± 173	1629 ± 161	1518 ± 117	1206 ± 102
204697_s_at	CHGA	chromogranin A	-0.0921	0.0243	-0.3461	0.2845	0.1283	1633 ± 242	1343 ± 329	960 ± 186	972 ± 118
204591_at	CHL1	cell adhesion molecule with homology to L1CAM	-0.0507	0.0103	0.4956	-0.2089	0.0491	1953 ± 265	1870 ± 314	1710 ± 211	970 ± 202
201569_s_at	CHN1	chimerin 1	-0.0099	0.0054	-0.4190	0.4325	0.0657	249 ± 25	249 ± 14	205 ± 23	173 ± 14
214665_s_at	CHP	calcium binding protein P22	-0.0504	0.0411	0.3693	0.3649	0.1622	1473 ± 178	1461 ± 209	1035 ± 124	1082 ± 201
200884_at	CKB	creatine kinase, brain	-0.1076	0.0380	0.0523	0.4316	0.3358	4370 ± 295	4522 ± 248	4302 ± 434	3598 ± 438
202712_s_at	CKMT1	creatine kinase, mitochondrial 1	-0.1097	0.0103	-0.4046	0.4797	0.1204	1283 ± 145	1158 ± 166	1060 ± 187	749 ± 93
204170_s_at	CKS2	CDC28 protein kinase 2	-0.0239	0.2937	-0.0140	0.1114	0.1372	225 ± 36	139 ± 12	191 ± 10	154 ± 31
212308_at	CLASP2	cytoplasmic linker associated protein 2	-0.1006	0.0364	0.0528	-0.1170	0.0391	1088 ± 119	1226 ± 103	1096 ± 80	796 ± 57
212306_at	CLDN10	claudin 10	-0.0008	0.0006	-0.0276	0.0899	0.0371	2139 ± 97	1732 ± 218	1741 ± 177	1395 ± 178
213415_at	CLIC2	chloride intracellular channel 2	-0.0493	0.0763	-0.0229	0.1437	0.0401	105 ± 30	30 ± 8	55 ± 15	24 ± 5
212358_at	CLIPR-59	CLIP-170-related protein	-0.2073	0.0011	-0.0029	0.2576	0.0076	4117 ± 165	3717 ± 244	3897 ± 334	2845 ± 187
205328_at	CLTC	clathrin, heavy polypeptide	-0.0275	0.0082	-0.3097	0.0867	0.0059	1243 ± 103	975 ± 50	847 ± 137	666 ± 105
206731_at	CNK2	connector enhancer of KSR2	-0.1118	0.0353	0.2282	0.2341	0.1553	862 ± 201	683 ± 164	411 ± 88	483 ± 108
200614_at	CNNM1	cyclin M1	-0.0037	0.0005	-0.4060	-0.2603	0.0410	7243 ± 670	6486 ± 304	5105 ± 392	5126 ± 842
220166_at	CNOT7	CCR4-NOT transcription complex, subunit 7	-0.0196	0.0047	-0.4636	0.4948	0.0024	616 ± 35	621 ± 78	523 ± 66	302 ± 20
218250_s_at	CNR1	cannabinoid receptor 1	-0.0004	0.0007	-0.1001	0.1061	0.0237	1628 ± 56	1649 ± 58	1422 ± 65	1344 ± 117

Web Table 5 (46)

Probe set	Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
219301_s_at	CNTNAP2	contactin associated protein-like 2	-0.0096	0.0561	-0.2951	0.2199	0.0670	629 ± 91	485 ± 73	339 ± 32	408 ± 89
211980_at	COL4A1	collagen, type IV, alpha 1	-0.0111	0.0357	-0.0599	0.0418	0.0339	689 ± 86	447 ± 65	423 ± 66	381 ± 79
221729_at	COL5A2	collagen, type V, α 2	0.0000	0.0007	-0.0116	0.0176	0.0000	4206 ± 290	1922 ± 298	766 ± 124	1310 ± 522
221730_at	COP9	COP9 homolog	-0.0096	0.0051	-0.0944	0.1228	0.0000	1659 ± 134	724 ± 123	195 ± 45	456 ± 222
208684_at	COPA	coatamer protein complex, subunit α	-0.0473	0.3604	-0.4467	-0.1221	0.6131	1527 ± 68	1631 ± 56	1440 ± 142	1457 ± 109
218042_at	COPS4	COP9 constitutive photomorphogenic homolog subunit 4	-0.0414	0.0530	0.4664	0.1270	0.1017	1411 ± 162	1218 ± 149	929 ± 87	1040 ± 166
201652_at	COPS5	COP9 constitutive photomorphogenic homolog subunit 5	-0.0029	0.1119	-0.0347	0.4678	0.2415	1170 ± 60	1079 ± 167	885 ± 84	916 ± 27
202142_at	COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A	-0.0366	0.0154	-0.1159	-0.2309	0.0287	1267 ± 78	1187 ± 102	930 ± 80	1000 ± 75
209029_at	COX11	COX11 homolog, cytochrome c oxidase assembly protein	-0.0187	0.0086	0.4964	-0.4636	0.0642	1094 ± 75	1102 ± 102	1009 ± 74	797 ± 87
211727_s_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	-0.0002	0.0008	-0.0663	0.4055	0.0520	627 ± 86	578 ± 87	492 ± 48	330 ± 42
203663_s_at	COX5A	cytochrome c oxidase subunit Va	-0.0477	0.3337	-0.4746	-0.2231	0.3107	2564 ± 323	2615 ± 373	1815 ± 166	2233 ± 436
211025_x_at	COX5B	cytochrome c oxidase subunit Vb	-0.0171	0.0881	-0.2443	-0.3922	0.2762	3810 ± 296	3875 ± 584	3088 ± 274	2881 ± 326
200086_s_at	COX6A1	cytochrome c oxidase subunit VIA polypeptide 1	-0.0001	0.0005	-0.1103	0.3323	0.0099	4745 ± 303	4355 ± 244	4522 ± 295	3153 ± 438
200925_at	COX6B	cytochrome c oxidase subunit Vlb	-0.0087	0.0019	-0.1796	0.1680	0.0020	12723 ± 648	1497 ± 1254	10636 ± 698	7477 ± 34
201441_at	COX6C	cytochrome c oxidase subunit Vlc	-0.0011	0.0045	-0.4819	0.4836	0.0084	3088 ± 164	2698 ± 207	2729 ± 175	2067 ± 36
201597_at	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2	-0.0016	0.0510	-0.4257	-0.1955	0.0486	5682 ± 223	5448 ± 435	5574 ± 386	4261 ± 165
201754_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	-0.0365	0.0106	0.2968	0.0477	0.0241	7154 ± 660	6528 ± 778	4910 ± 480	4418 ± 813
201256_at	COX7B	cytochrome c oxidase subunit VIlb	-0.0042	0.0011	-0.4572	-0.4843	0.0134	2624 ± 221	2158 ± 70	1833 ± 81	1970 ± 221
213846_at	COX7C	cytochrome c oxidase subunit VIlc	-0.0033	0.0009	-0.2401	0.0316	0.0021	1180 ± 99	916 ± 81	841 ± 31	748 ± 66
201119_s_at	CPNE6	cytochrome c oxidase subunit VIII	-0.0387	0.0862	-0.4139	0.2828	0.2939	2745 ± 212	2695 ± 174	2211 ± 241	2146 ± 419
210408_s_at	CPNE5	copine VI	-0.0711	0.0434	0.2474	0.2488	0.2977	805 ± 117	738 ± 161	631 ± 87	490 ± 74
201134_x_at	CPSF5	cleavage and polyadenylation specific factor 6, 68kDa	-0.0285	0.0352	0.0873	-0.0800	0.1328	4528 ± 388	4138 ± 386	3705 ± 372	3135 ± 494
202469_s_at	CRH	corticotropin releasing hormone	-0.0235	0.0378	0.2689	0.0300	0.0032	445 ± 21	475 ± 20	482 ± 10	348 ± 36
205630_at	CR11	CREBBP/EP300 inhibitory protein 1	-0.0206	0.0113	-0.3332	-0.3983	0.0581	247 ± 48	186 ± 39	108 ± 10	154 ± 21
202551_s_at	CRIM1	cysteine-rich motor neuron 1	-0.0068	0.0796	-0.1490	-0.0470	0.0951	701 ± 55	659 ± 55	650 ± 64	494 ± 56
208669_s_at	CRMP1	collapse response mediator protein 1	-0.0489	0.0212	0.4501	0.1914	0.0455	1687 ± 244	1599 ± 311	1072 ± 114	835 ± 143
202517_at	CRNKL1	Crm, crooked neck-like 1	-0.0033	0.0014	-0.1276	0.1445	0.2375	1857 ± 55	1938 ± 205	1651 ± 187	1501 ± 153
221517_s_at	CRSP6	cofactor required for Sp1 transcriptional activation, subunit 6	-0.1315	0.0491	-0.0479	-0.4372	0.0973	315 ± 24	267 ± 28	228 ± 17	201 ± 54
205489_at	CRYM	crystallin, mu	-0.1000	0.0105	0.2397	0.2176	0.0930	2634 ± 628	2301 ± 413	2238 ± 440	944 ± 114
219913_s_at	CRYZ	crystallin, zeta	-0.0108	0.0004	-0.1169	0.3803	0.0197	631 ± 27	605 ± 56	546 ± 25	456 ± 34
208660_at	CS	citrate synthase	-0.1882	0.0473	-0.1043	0.3386	0.3413	2407 ± 105	2485 ± 164	2251 ± 147	2168 ± 97
202950_at	CSE1L	CSE1 chromosome segregation 1-like	-0.0306	0.0259	0.3843	-0.0611	0.0128	538 ± 53	502 ± 70	399 ± 49	266 ± 34
201112_s_at	CSNK1G3	casein kinase 1, γ 3	-0.0247	0.0095	-0.0112	0.0262	0.0255	1033 ± 76	1145 ± 116	881 ± 60	779 ± 46
20768_s_at	CSNK2A1	casein kinase 2, α 1 polypeptide	-0.0100	0.0104	-0.0453	0.2267	0.0277	368 ± 22	297 ± 25	303 ± 13	271 ± 30
205143_at	CSPG3	chondroitin sulfate proteoglycan 3	-0.1035	0.0019	0.0768	-0.3863	0.0046	3646 ± 284	4419 ± 457	3632 ± 352	2396 ± 230
206075_s_at	CSPG5	chondroitin sulfate proteoglycan 5	-0.0231	0.0028	-0.3590	-0.2245	0.0423	431 ± 17	386 ± 20	359 ± 40	289 ± 47
205373_at	CTNNA2	catenin, α 2	-0.0821	0.0434	0.2489	-0.3519	0.1447	1375 ± 150	1337 ± 202	1309 ± 249	772 ± 182
207614_s_at	CUL1	cullin 1	-0.0760	0.0394	-0.0723	0.1441	0.0406	749 ± 47	605 ± 54	547 ± 30	557 ± 84
39966_at	CUL2	cullin 2	-0.0179	0.0012	-0.2967	0.0206	0.0009	4013 ± 159	4238 ± 394	4309 ± 330	2498 ± 302

Web Table 5 (47)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
203079_s_at	CXCL14	chemokine ligand 14	-0.0181	0.0129	-0.3447	0.0778	0.0190	431 ± 28	382 ± 40	331 ± 17	304 ± 29
201828_x_at	CXX1	CAAX box 1	-0.0429	0.0994	0.3519	0.0817	0.3273	6288 ± 695	6106 ± 505	4886 ± 517	5410 ± 580
201066_at	CYC1	cytochrome c-1	-0.0331	0.2562	-0.4541	-0.4342	0.2587	1110 ± 98	1027 ± 71	858 ± 65	975 ± 116
204716_at	D10S170	DNA segment on chromosome 10 170	-0.0329	0.0615	0.2104	0.2419	0.2427	434 ± 16	415 ± 32	417 ± 31	347 ± 45
208872_s_at	D5S346	DNA segment, single copy probe LNS-CAI/LNS-CAII	-0.0067	0.0407	-0.1455	0.4736	0.1083	681 ± 58	591 ± 54	524 ± 46	495 ± 68
208873_s_at	dbA141HS.1	similar to neuralin 1	-0.0002	0.0003	-0.1752	0.2336	0.1670	4398 ± 307	3919 ± 387	3731 ± 291	3318 ± 379
205818_at	DBCCR1	deleted in bladder cancer chromosome region candidate 1	-0.0612	0.0406	0.4569	0.2781	0.2044	1115 ± 137	957 ± 154	780 ± 112	791 ± 96
209763_at	DC6	DC6 protein	-0.0130	0.0018	-0.2837	0.2859	0.0029	576 ± 33	505 ± 54	436 ± 44	335 ± 38
218482_at	DCTN2	dynactin 2	-0.0211	0.0050	-0.3244	0.4498	0.0158	579 ± 55	545 ± 64	470 ± 33	335 ± 55
200932_s_at	DDOST	1,6-bisphosphoglucoamylase	-0.0167	0.0102	-0.4887	-0.2150	0.0238	1164 ± 85	1134 ± 92	994 ± 61	814 ± 62
202929_s_at	DDT	D-dopachrome tautomerase	-0.0197	0.1039	0.3307	-0.2800	0.1649	351 ± 26	390 ± 42	301 ± 22	241 ± 78
208875_s_at	DDX1	DEAD/H box polypeptide 1	-0.0016	0.0043	-0.0671	0.4050	0.0313	835 ± 61	858 ± 98	730 ± 48	567 ± 42
200033_at	DDX5	DEAD/H box polypeptide 5	-0.0471	0.5049	-0.0209	0.3871	0.6756	4816 ± 211	4787 ± 203	4361 ± 380	4314 ± 594
209407_s_at	DEAF1	deformed epidermal autoregulatory factor 1	-0.0458	0.0854	-0.0015	0.0319	0.1909	1447 ± 115	1121 ± 108	1175 ± 121	1145 ± 139
207431_s_at	DEGS	degenerative spermatocyte homolog, lipid desaturase	-0.0142	0.1882	-0.4856	-0.1448	0.2535	343 ± 28	413 ± 54	333 ± 42	278 ± 53
220482_s_at	DELGEF	putative guanine nucleotide exchange factor	-0.0037	0.1192	0.1919	-0.4365	0.0541	161 ± 12	154 ± 20	168 ± 18	101 ± 20
216307_at	DGKB	diacylglycerol kinase, β 90kDa	-0.3368	0.0304	-0.3492	0.1441	0.2894	191 ± 11	202 ± 31	188 ± 23	142 ± 10
201241_at	DGUOK	deoxyguanosine kinase	-0.0050	0.1341	-0.1588	0.4425	0.2613	1351 ± 68	1201 ± 145	980 ± 73	936 ± 112
201790_s_at	DHCR7	7-dehydrocholesterol reductase	-0.0023	0.0063	0.3178	0.2036	0.0005	676 ± 80	723 ± 98	565 ± 26	513 ± 92
203816_at	DIO2	deiodinase, iodothyronine, type II	-0.0174	0.0025	0.3598	-0.4399	0.0202	196 ± 21	228 ± 14	162 ± 22	72 ± 28
203700_s_at	DI-Ras2	Di-Ras2	-0.3097	0.0268	0.4711	-0.4529	0.2396	533 ± 50	497 ± 39	404 ± 46	332 ± 40
213149_at	DLAT	dihydrolipoamide S-acyltransferase	-0.0217	0.0181	0.4689	0.2180	0.2533	465 ± 44	418 ± 69	438 ± 16	316 ± 68
213617_s_at	OLD	dihydrolipoamide dehydrogenase	-0.0854	0.0038	-0.1550	0.4551	0.0449	434 ± 33	405 ± 43	353 ± 58	323 ± 26
206253_at	DLG2	discs, large homolog 2, chapsyn-110	-0.0651	0.0174	-0.4121	0.2295	0.0324	195 ± 21	191 ± 11	139 ± 17	134 ± 20
206489_s_at	DLGAP1	discs, large homolog-associated protein 1	-0.0206	0.0009	-0.0275	0.2242	0.1371	125 ± 21	99 ± 14	61 ± 14	71 ± 6
209095_at	DLGAP2	discs, large homolog-associated protein 2	-0.0190	0.0036	-0.3302	0.3555	0.0238	1235 ± 225	1096 ± 130	916 ± 101	690 ± 143
210227_at	DMD	dystrophin	-0.0115	0.0951	-0.0059	0.4265	0.0987	1305 ± 73	1150 ± 147	1015 ± 128	789 ± 76
200881_s_at	DNAJA1	DnaJ homolog, subfamily A, member 1	-0.0115	0.0951	-0.0059	0.4265	0.0987	1620 ± 249	1215 ± 132	1296 ± 172	903 ± 68
203881_s_at	DNAJB9	DnaJ homolog, subfamily B, member 9	-0.0066	0.0055	-0.3755	0.1129	0.0112	1080 ± 110	932 ± 42	765 ± 63	701 ± 69
204720_s_at	DNAJC6	DnaJ homolog, subfamily C, member 6	-0.0200	0.0663	-0.1231	-0.2312	0.1939	5519 ± 319	5305 ± 691	5030 ± 218	4098 ± 632
212490_at	DNAJC8	DnaJ homolog, subfamily C, member 8	-0.2041	0.0406	0.2941	0.0026	0.0437	276 ± 20	215 ± 16	261 ± 22	200 ± 22
211928_at	DNCH1	dynein, cytoplasmic, heavy polypeptide 1	-0.2795	0.0277	-0.1075	0.3555	0.0799	3656 ± 126	3325 ± 273	3588 ± 248	2797 ± 306
202842_s_at	DNCL1	dynein, cytoplasmic, intermediate polypeptide 1	-0.0185	0.0009	0.3331	0.1874	0.0114	1925 ± 161	1839 ± 66	1375 ± 95	1469 ± 139
211684_s_at	DNCL2	dynein, cytoplasmic, intermediate polypeptide 2	-0.0399	0.3712	-0.1479	-0.1333	0.2865	2985 ± 92	2999 ± 331	3062 ± 257	2484 ± 172
205348_s_at	DNCL1	dynein, cytoplasmic, light intermediate polypeptide 1	-0.0206	0.0459	-0.3530	0.3640	0.0100	2489 ± 291	2366 ± 267	1631 ± 112	1493 ± 153
217916_at	DNLC2A	dynein light chain 2A	-0.2113	0.0387	-0.1272	-0.4797	0.1685	5575 ± 232	5027 ± 711	4537 ± 355	4209 ± 500
217976_s_at	DNM1L	dynamitin 1-like	-0.0059	0.0020	-0.0611	0.2493	0.1058	545 ± 67	465 ± 58	352 ± 48	347 ± 86
203105_s_at	DOCK3	dedicator of cyto-kinesis 3	-0.0162	0.0028	-0.1914	0.3169	0.0031	403 ± 27	351 ± 24	292 ± 10	272 ± 35
213482_at	DRAP1	DR1-associated protein 1	-0.0156	0.0137	-0.0392	-0.4163	0.0241	521 ± 80	421 ± 74	350 ± 43	202 ± 74

Web Table 5 (48)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
204751_x_at DSC2	desmocollin 2	-0.0377	-0.8438	-0.2203	0.0944	0.7515	100 ± 11	94 ± 10	84 ± 7	101 ± 20
203498_at DSCR1L1	Down syndrome critical region gene 1-like 1	-0.1169	0.0130	-0.4289	0.2339	0.0768	1848 ± 291	1701 ± 249	1650 ± 226	971 ± 95
203405_at DSCR2	Down syndrome critical region gene 2	-0.0060	0.1123	0.3201	0.2474	0.2319	427 ± 28	423 ± 26	349 ± 26	381 ± 42
221889_s_at DSCR5	Down syndrome critical region gene 5	-0.0023	0.1583	-0.4931	-0.3598	0.0686	828 ± 44	892 ± 57	701 ± 42	772 ± 56
202276_at DSS1	Deleted in split-hand/split-foot 1 region	-0.0445	0.3622	0.1571	-0.3598	0.6194	524 ± 33	524 ± 14	456 ± 21	486 ± 72
209457_at DUSP5	dual specificity phosphatase 5	-0.0034	0.2196	-0.0655	0.1422	0.0493	291 ± 32	245 ± 27	153 ± 30	229 ± 47
203258_at DUSP6	dual specificity phosphatase 6	-0.0342	0.0142	0.1622	0.1439	0.0287	762 ± 50	617 ± 106	573 ± 57	419 ± 82
202348_s_at DYT1	dystonia 1, torsion	-0.1608	0.0200	0.4272	0.2288	0.1102	366 ± 32	362 ± 31	277 ± 23	298 ± 34
208891_at DZIP1	zinc-finger protein DZIP1	-0.0327	0.0259	-0.1200	-0.3969	0.0438	1130 ± 189	832 ± 37	752 ± 113	564 ± 118
204557_s_at E2IG5	hypothetical protein, estradiol-induced	-0.0003	0.0027	-0.2519	0.3703	0.0327	625 ± 28	538 ± 83	593 ± 62	389 ± 39
220842_x_at E46L	like mouse brain protein E46	-0.0028	0.0199	-0.1262	0.1473	0.0098	1915 ± 143	1728 ± 181	1292 ± 104	1290 ± 174
202735_at EBP	emopamil binding protein	-0.4425	0.0342	0.0171	-0.1000	0.1573	185 ± 17	188 ± 15	179 ± 13	136 ± 22
200789_at ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	-0.0045	0.0751	-0.0010	0.1452	0.2163	795 ± 40	728 ± 41	688 ± 26	651 ± 85
219787_s_at ECT2	epithelial cell transforming sequence 2 oncogene	-0.0435	0.6363	0.2683	-0.2427	0.4048	155 ± 20	155 ± 12	118 ± 20	147 ± 15
204642_at EDG1	sphingolipid G-protein-coupled receptor 1	-0.1163	0.0444	0.3601	-0.3498	0.0494	975 ± 67	1023 ± 124	979 ± 87	687 ± 60
208399_s_at EDN3	endothelin 3	-0.0572	0.0134	0.0593	-0.4652	0.0590	144 ± 36	162 ± 23	74 ± 19	71 ± 24
204905_s_at EEFE1E1	eukaryotic translation elongation factor 1 epsilon 1	-0.0243	0.1460	-0.4260	0.4063	0.3245	515 ± 45	440 ± 62	392 ± 45	393 ± 71
208833_s_at EFA6R	ADP-ribosylation factor guanine nucleotide factor 6	-0.0203	0.0074	-0.3761	-0.4133	0.0077	3421 ± 300	2758 ± 228	2011 ± 182	2483 ± 358
203354_s_at EFN82	ephrin-B2	-0.0024	0.0004	-0.1873	0.1572	0.0574	595 ± 43	624 ± 138	507 ± 62	303 ± 39
201632_at EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 α	-0.0166	0.1292	-0.0242	0.1385	0.1055	1099 ± 39	994 ± 24	897 ± 73	920 ± 85
202668_at EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 γ	-0.0017	0.0221	-0.0174	0.2218	0.0004	1863 ± 123	1516 ± 91	1329 ± 68	1216 ± 99
218488_at EIF2S1	eukaryotic translation initiation factor 2, subunit 1 α	-0.0392	0.0341	0.3705	-0.3375	0.0271	443 ± 41	406 ± 23	303 ± 13	328 ± 50
200005_at EIF3S7	eukaryotic translation initiation factor 3, subunit 7 zeta	-0.0430	0.1540	-0.4749	-0.3078	0.1272	1140 ± 47	1175 ± 66	1128 ± 51	978 ± 55
206051_at ELAVL4	ELAV-like 4	-0.0733	0.0090	-0.3688	0.2806	0.0864	2362 ± 351	1887 ± 327	1753 ± 292	1205 ± 197
204513_s_at ELMO1	engulfment and cell motility 1	-0.0472	0.3646	-0.4274	-0.3889	0.5308	2231 ± 168	2110 ± 298	1841 ± 177	1803 ± 341
221528_s_at ELMO2	engulfment and cell motility 2	-0.2807	0.0498	-0.3200	0.0314	0.3301	828 ± 36	772 ± 70	732 ± 67	662 ± 86
208290_s_at ELOVL2	elongation of very long chain fatty acids-like 2	-0.0247	0.0418	0.1212	-0.0167	0.1245	492 ± 82	355 ± 52	329 ± 40	294 ± 44
219532_at ELOVL4	elongation of very long chain fatty acids-like 4	-0.0607	0.0470	0.4544	-0.1750	0.3105	566 ± 64	563 ± 75	512 ± 81	369 ± 99
213712_at ENC1	ectodermal-neural cortex	-0.0071	0.0102	-0.2900	0.2102	0.0564	415 ± 14	449 ± 74	395 ± 60	244 ± 46
201341_at ENO2	enolase 2,	-0.0277	0.0251	-0.3999	-0.2935	0.1253	9931 ± 1082	9003 ± 1360	1446 ± 1365	5447 ± 1794
201313_at ENSA	endosulfine α	-0.0079	0.0003	0.1580	0.2694	0.0973	3317 ± 330	3654 ± 583	2571 ± 323	2190 ± 436
202596_at ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	-0.0045	0.0020	-0.1906	0.0977	0.0021	1892 ± 235	1930 ± 187	1667 ± 152	821 ± 87
204505_s_at EPB49	erythrocyte membrane protein band 4.9	-0.0769	0.0035	-0.2731	0.3281	0.0213	1621 ± 180	1485 ± 155	1519 ± 132	965 ± 71
205114_at EPHA4	EphA4	-0.0806	0.0436	-0.3691	-0.2538	0.2281	579 ± 63	498 ± 82	382 ± 39	399 ± 117
208852_at EPHA7	EphA7	-0.0910	0.0373	0.2443	-0.3807	0.0280	66 ± 7	76 ± 21	31 ± 3	37 ± 9
209589_s_at EPHB2	EphB2	-0.0852	0.0341	0.3128	0.0661	0.2759	176 ± 17	185 ± 29	172 ± 25	123 ± 10
217886_at EPS15	epidermal growth factor receptor pathway substrate 15	-0.0406	0.0624	0.4171	0.4492	0.0388	2459 ± 163	2233 ± 129	1809 ± 102	2056 ± 221
203009_at ESD	esterase D-formylglutathione hydrolase	-0.0060	0.0958	-0.3487	-0.1029	0.1337	2421 ± 100	2433 ± 275	2068 ± 72	1935 ± 210
205191_at ETFA	electron-transfer-flavoprotein, α polypeptide	-0.0028	0.0209	0.4758	-0.3541	0.0071	782 ± 78	642 ± 89	465 ± 31	476 ± 54

Web Table 5 (49)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
201329_s_at	ETS2	-0.0614	0.0132	0.4498	-0.2522	0.0077	276 ± 10	312 ± 27	290 ± 20	208 ± 11
201931_at	F8	-0.0019	0.0017	-0.3895	0.2345	0.0249	581 ± 34	579 ± 19	481 ± 30	459 ± 42
205756_s_at	F8A	-0.0057	0.0081	-0.3027	0.1887	0.0388	750 ± 29	728 ± 47	687 ± 44	576 ± 47
205739_s_at	FABP3	-0.3339	0.0366	0.0435	-0.4552	0.3537	322 ± 37	323 ± 39	272 ± 19	250 ± 36
203274_at	FABP7	-0.0104	0.0071	-0.1157	0.1640	0.0371	1569 ± 149	1331 ± 153	1151 ± 71	1014 ± 136
205029_s_at	FACL3	-0.0053	0.0094	-0.3508	0.4110	0.0517	689 ± 100	643 ± 110	534 ± 99	286 ± 101
204283_at	FARS1	-0.0108	0.1441	0.4891	0.3153	0.3641	202 ± 18	187 ± 14	159 ± 21	162 ± 25
214436_at	FBXL2	-0.0577	0.0035	-0.3235	-0.4576	0.0286	883 ± 55	796 ± 63	737 ± 66	625 ± 44
212231_at	FBXO21	-0.0429	0.0590	-0.4226	0.4384	0.3762	1295 ± 70	1346 ± 151	1174 ± 130	1057 ± 127
201662_s_at	FBXO3	-0.0057	0.0164	-0.4662	-0.2358	0.0429	973 ± 113	876 ± 95	747 ± 86	569 ± 90
218751_s_at	FBXW7	-0.1629	0.0077	0.4004	-0.4998	0.0474	1404 ± 220	1282 ± 188	1257 ± 193	613 ± 50
204232_at	FCERTG	-0.0190	0.1445	-0.0266	0.3763	0.1576	1292 ± 193	1037 ± 91	944 ± 58	921 ± 83
216950_s_at	FCGR1A	-0.0493	0.1039	-0.1366	-0.2976	0.3182	391 ± 75	380 ± 42	274 ± 43	264 ± 53
218432_at	FECH	-0.0224	0.0394	-0.4570	0.4527	0.0373	864 ± 74	786 ± 110	652 ± 59	544 ± 70
203116_s_at	FGF13	-0.0071	0.0121	-0.4317	0.3058	0.1240	626 ± 34	652 ± 30	557 ± 29	550 ± 43
214170_x_at	FH	-0.0431	0.2927	0.2571	0.2846	0.5091	936 ± 135	839 ± 83	729 ± 50	789 ± 106
208492_at	FHIT	-0.0156	0.3462	-0.4097	-0.3905	0.4292	318 ± 18	323 ± 21	268 ± 24	277 ± 49
214505_s_at	FHL1	-0.2094	0.0486	0.3758	0.0415	0.2475	526 ± 76	515 ± 94	329 ± 38	387 ± 96
204380_s_at	FIBP	-0.0448	0.0032	0.3180	0.1246	0.0747	149 ± 23	142 ± 21	114 ± 25	68 ± 17
202041_s_at	FKBP1B	-0.0074	0.0218	0.2725	0.0184	0.0441	1083 ± 84	1009 ± 58	952 ± 54	791 ± 51
208657_s_at	FKBP3	-0.0498	0.0081	-0.3837	-0.4594	0.0794	2493 ± 299	2116 ± 186	1592 ± 196	1751 ± 286
219499_at	FLJ10578	-0.0565	0.0499	0.4279	0.3337	0.0856	463 ± 44	475 ± 48	354 ± 17	374 ± 30
218175_at	FLJ22471	-0.1001	0.0187	0.1973	0.1228	0.2449	7621 ± 380	8391 ± 909	7113 ± 632	6512 ± 599
204359_at	FLRT2	-0.2159	0.0206	0.4729	0.3440	0.0658	1599 ± 190	1325 ± 109	1140 ± 111	1063 ± 147
218003_s_at	FN1	-0.0397	0.0035	0.2565	0.1299	0.0349	1565 ± 83	1395 ± 113	1388 ± 74	1160 ± 99
206018_at	FOXG1B	-0.0423	0.0667	-0.2474	0.4724	0.2127	3556 ± 390	3137 ± 432	2699 ± 248	2537 ± 398
210495_x_at	FRG1	-0.0149	0.0274	0.3979	0.2650	0.0073	1804 ± 201	1582 ± 146	1640 ± 107	983 ± 132
219170_at	FSD1	-0.3995	0.0208	-0.0207	0.1889	0.1650	1016 ± 65	848 ± 121	823 ± 106	703 ± 101
215160_x_at	FSTL1	-0.0003	0.0012	0.4544	0.3929	0.0525	314 ± 13	326 ± 21	254 ± 31	260 ± 16
208310_s_at	FTS	-0.0432	0.0221	0.3415	0.2117	0.0057	356 ± 28	350 ± 22	269 ± 25	234 ± 28
202838_at	FUCA1	-0.0248	0.1201	0.0782	-0.3119	0.2657	472 ± 33	505 ± 49	450 ± 44	368 ± 65
218373_at	FXYD6	-0.0200	0.0172	-0.2737	0.3411	0.1226	1474 ± 182	1319 ± 135	1136 ± 123	937 ± 182
217897_at	FXYD7	-0.0485	0.0032	0.4744	0.3027	0.0432	3867 ± 465	2976 ± 473	2667 ± 450	2124 ± 184
220131_at	G3BP2	-0.0141	0.0406	-0.4220	0.3561	0.0621	867 ± 103	991 ± 135	762 ± 108	544 ± 83
208841_s_at	GAA	-0.0172	0.0150	0.1570	0.4393	0.1857	2239 ± 241	2019 ± 275	1669 ± 144	1563 ± 300
202812_at	GABBR1	-0.0382	0.0016	0.1947	0.3817	0.1572	655 ± 18	555 ± 48	578 ± 37	551 ± 48
207014_at	GABRA2	-0.0578	0.0232	0.2467	-0.3925	0.1946	528 ± 60	505 ± 113	402 ± 69	301 ± 78
205850_s_at	GABRB3	-0.0089	0.0515	-0.3541	0.0264	0.3529	157 ± 17	138 ± 24	111 ± 15	118 ± 26
203146_s_at	GAD1	-0.0057	0.0160	-0.0682	0.0892	0.0075	4399 ± 399	5093 ± 551	4248 ± 492	2697 ± 208

Web Table 5 (50)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
205278_at	GAD2	glutamate decarboxylase 2	-0.0365	0.0336	-0.1256	0.1361	0.0413	2633 ± 303	1633 ± 340	1489 ± 285	1401 ± 437
204417_at	GALC	galactosylceramidase	-0.0243	0.2171	-0.4908	-0.2056	0.3357	1253 ± 48	1293 ± 140	1110 ± 59	1123 ± 67
206780_at	GALGT	galactosylglucosylceramide N-acetylglucosaminyltransferase	-0.0456	0.0014	0.3795	0.0130	0.0114	1015 ± 92	657 ± 96	458 ± 101	641 ± 156
206435_at	GAP43	growth associated protein 43	-0.0098	0.0037	-0.2652	0.1629	0.0116	647 ± 76	501 ± 61	407 ± 47	388 ± 21
204471_at	GAPD	glyceraldehyde-3-phosphate dehydrogenase	-0.0463	0.0129	-0.1279	0.3797	0.0320	2527 ± 419	1819 ± 315	1326 ± 238	1093 ± 388
213453_x_at	GBAS	glioblastoma amplified sequence	-0.0047	0.0148	0.2472	-0.3722	0.0306	14914 ± 757	4494 ± 1121	14695 ± 766	0854 ± 4435
201738_at	GC20	translation factor su11 homolog	-0.0831	0.0334	-0.2666	0.1112	0.2023	2748 ± 223	2633 ± 124	2225 ± 100	2088 ± 421
204224_s_at	GCH1	GTP cyclohydrolase 1	-0.0093	0.1634	-0.1284	0.4031	0.1779	230 ± 11	187 ± 13	202 ± 11	176 ± 30
214005_at	GGCX	γ-glutamyl carboxylase	-0.0827	0.0167	0.0169	0.3015	0.0605	216 ± 16	242 ± 35	215 ± 21	147 ± 7
209248_at	GHITM	growth hormone inducible transmembrane protein	-0.0187	0.0324	-0.1177	0.3383	0.0615	3766 ± 500	3188 ± 361	2607 ± 259	2286 ± 891
219137_s_at	GL004	GL004 protein	-0.0894	0.0360	-0.1503	0.0771	0.1230	1403 ± 91	1335 ± 46	1108 ± 99	1114 ± 156
200881_at	GLO1	glyoxalase I	-0.0240	0.0961	-0.3395	0.3674	0.2520	2702 ± 217	2459 ± 274	2065 ± 198	2124 ± 346
209249_s_at	GLRB	glycine receptor, β	-0.0316	0.0299	-0.4064	0.2521	0.0758	2140 ± 265	1815 ± 264	1352 ± 127	1365 ± 297
206652_at	GLRX	glutaredoxin	-0.0728	0.0340	-0.4513	0.0457	0.0196	1484 ± 231	829 ± 69	846 ± 76	829 ± 66
203158_s_at	GLS	glutaminase	-0.0238	0.0149	-0.2128	0.3964	0.0057	369 ± 40	282 ± 19	238 ± 15	223 ± 31
200947_s_at	GLUD1	glutamate dehydrogenase 1	-0.0132	0.0043	-0.2764	0.1425	0.0164	3533 ± 227	3447 ± 269	3268 ± 157	2427 ± 214
200946_x_at	GLUD2	Glutamate dehydrogenase-2	-0.0138	0.0113	-0.4296	0.3589	0.0293	2361 ± 224	2204 ± 226	2169 ± 231	1452 ± 124
215794_x_at	GLUL	glutamate-aminonia ligase	-0.0324	0.0321	-0.0247	0.4324	0.0429	773 ± 90	686 ± 96	530 ± 31	485 ± 10
200648_s_at	GNA14	guanine nucleotide binding protein, α 14	-0.0268	0.0005	-0.1397	-0.1009	0.0844	2336 ± 499	1694 ± 273	1658 ± 161	978 ± 281
220108_at	GNA1	G protein, α activating activity polypeptide, olfactory type	-0.0085	0.0126	0.1015	0.3239	0.0000	324 ± 22	346 ± 18	330 ± 26	139 ± 32
206355_at	GNAO1	G-protein, α activating activity polypeptide O	-0.0046	0.0088	-0.2666	-0.4524	0.0962	373 ± 43	369 ± 41	325 ± 25	242 ± 40
212273_x_at	GNAS	GNAS complex locus	-0.0306	0.0024	-0.0022	0.0457	0.0151	15346 ± 513	12684 ± 969	13037 ± 942	0407 ± 1560
200744_s_at	GNB1	guanine nucleotide binding protein, β polypeptide 1	-0.0382	0.0271	-0.0395	0.1740	0.1601	662 ± 73	474 ± 52	538 ± 58	482 ± 70
200745_s_at	GNG3	guanine nucleotide binding protein, γ 3	-0.0438	0.0026	0.3629	0.4306	0.1644	3025 ± 216	2635 ± 201	2490 ± 136	2385 ± 290
222005_s_at	GOLGIN-67	golgin-67	0.0000	0.0012	-0.2590	0.4586	0.0265	1904 ± 212	1866 ± 278	1615 ± 235	908 ± 115
208843_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	-0.0307	0.2282	0.0177	-0.0397	0.2384	1527 ± 62	1706 ± 66	1525 ± 55	1460 ± 136
208798_x_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble	-0.0213	0.0129	-0.3284	0.2218	0.0516	1634 ± 134	1319 ± 108	1349 ± 188	978 ± 206
208813_at	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial	-0.0001	0.0276	-0.4403	-0.1149	0.0628	1289 ± 242	987 ± 207	671 ± 139	546 ± 206
211060_x_at	GPAA1	GPAA1P anchor attachment protein 1 homolog	-0.0332	0.0627	0.2325	0.4906	0.2260	823 ± 51	843 ± 100	751 ± 70	639 ± 41
200708_at	GPC5	glypican 5	-0.0218	0.0169	0.0578	0.3800	0.0222	2442 ± 80	2450 ± 260	1863 ± 149	1913 ± 147
208308_s_at	GPI	glucose phosphate isomerase	-0.0830	0.0070	-0.0721	0.3316	0.0886	3211 ± 320	2880 ± 412	2543 ± 252	1965 ± 388
209469_at	GPM6A	glycoprotein M6A	-0.0599	0.0113	-0.3806	-0.3004	0.0519	8482 ± 449	8256 ± 723	8168 ± 941	5772 ± 770
221288_at	GPR22	G protein-coupled receptor 22	-0.0612	0.0004	-0.2999	0.0149	0.0054	335 ± 43	240 ± 40	141 ± 30	152 ± 48
208470_s_at	GPR51	G protein-coupled receptor 51	-0.0178	0.0038	-0.2145	0.3256	0.0334	8036 ± 601	7569 ± 1000	6653 ± 847	4586 ± 876
209890_s_at	GRIA1	glutamate receptor, ionotropic, AMPA 1	-0.0048	0.0018	-0.4705	0.1291	0.0470	5017 ± 552	4018 ± 595	3662 ± 651	2590 ± 496
205358_at	GRIA2	glutamate receptor, ionotropic, AMPA 2	-0.3308	0.0212	-0.4981	0.1884	0.1726	7425 ± 317	7290 ± 456	7576 ± 717	5752 ± 860
209793_at	GRIA3	glutamate receptor, ionotropic, AMPA 3	-0.0082	0.0078	-0.4700	-0.0656	0.0099	2199 ± 276	1690 ± 389	993 ± 98	1055 ± 232
206730_at	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	-0.0076	0.0200	-0.4489	-0.1211	0.0056	418 ± 23	513 ± 60	330 ± 34	297 ± 43
205541_s_at	GSPT2	G1 to S phase transition 2	-0.0554	0.0482	-0.2396	0.1623	0.0653	688 ± 62	493 ± 77	483 ± 36	471 ± 85

Web Table 5 (51)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
206534_at GSTA4	glutathione S-transferase A4	-0.0037	0.0104	-0.2958	0.3293	0.0464	224 ± 30	262 ± 50	154 ± 34	112 ± 26
202554_s_at GSTM3	glutathione S-transferase M3	-0.0494	0.5239	0.3724	-0.1898	0.5830	1344 ± 137	1484 ± 233	1133 ± 190	1206 ± 170
202967_at GSTTLp28	GST like: glutathione transferase omega	-0.0039	0.0238	-0.2333	0.3244	0.0393	1906 ± 167	1579 ± 177	1373 ± 177	1230 ± 148
202670_at GTF2A2	general transcription factor IIA, 2, 12kDa	-0.0174	0.1775	-0.0760	0.0448	0.1555	825 ± 39	670 ± 49	635 ± 64	683 ± 89
201470_at GUCY1B3	guanylate cyclase 1, soluble, β 3	-0.0192	0.0057	-0.4297	0.2103	0.1335	2576 ± 113	2481 ± 163	2180 ± 147	2180 ± 172
203817_at GUK1	guanylate kinase 1	-0.0070	0.0084	0.2298	0.0799	0.0306	2116 ± 325	1694 ± 248	1201 ± 176	1128 ± 205
200075_s_at GW128	GW128 protein	-0.0218	0.0216	-0.2739	0.2388	0.0972	2769 ± 282	2417 ± 185	2167 ± 104	1947 ± 385
207169_s_at H2AFY	H2A histone family, member Y	-0.1291	0.0403	0.4183	-0.3448	0.1239	2313 ± 103	2354 ± 77	2015 ± 99	1983 ± 324
211569_s_at HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-0.2232	0.0493	-0.0326	0.4335	0.2136	323 ± 24	333 ± 17	286 ± 24	272 ± 17
217718_s_at HAPIP	huntingtin-associated protein interacting protein	-0.0360	0.0099	-0.4800	0.2452	0.2347	11085 ± 706	10473 ± 927	9320 ± 633	8682 ± 1920
205635_at HARP11	uncharacterized hypothalamus protein HARP11	-0.0209	0.0174	-0.4418	0.1694	0.0648	1278 ± 131	1066 ± 130	923 ± 98	855 ± 96
204018_x_at HBA1	hemoglobin, α 1	-0.1249	0.0122	0.0574	-0.2787	0.0051	4439 ± 1068	7014 ± 1153	4733 ± 561	1422 ± 369
211745_x_at HBA2	hemoglobin, α 2	-0.1882	0.0257	0.0684	-0.2924	0.0165	4677 ± 1127	7230 ± 1226	5047 ± 702	2120 ± 525
211698_x_at HBB	hemoglobin, β	-0.0567	0.0299	0.1455	-0.1629	0.0259	3914 ± 1009	5946 ± 1422	3800 ± 727	1259 ± 161
222230_s_at HBXIP	hepatitis B virus x interacting protein	-0.0452	0.0330	-0.3547	0.3908	0.0877	2093 ± 351	1677 ± 307	1216 ± 142	1178 ± 175
202300_at HCCA3	hepatocellular carcinoma susceptibility protein	-0.0064	0.0042	-0.2895	0.2019	0.0836	1516 ± 111	1377 ± 152	1137 ± 62	1147 ± 37
218467_at HCCS	holocytochrome c synthase	-0.0009	0.0072	-0.3093	-0.4453	0.0609	587 ± 37	552 ± 66	474 ± 20	419 ± 56
203745_at HCS	cytochrome c	-0.0075	0.0032	-0.0511	-0.2885	0.0341	5741 ± 469	5213 ± 723	4540 ± 314	3586 ± 502
208905_at HERC1	hect carboxyl terminus domain and RCC1-like domain 1	-0.0264	0.1259	-0.0589	-0.4307	0.4833	914 ± 68	869 ± 74	845 ± 64	762 ± 69
217902_s_at HERC2	hect domain and RLD 2	-0.0050	0.0543	-0.0906	0.1638	0.2112	602 ± 45	581 ± 24	504 ± 43	487 ± 56
201944_at HEXB	hexosaminidase B	-0.0400	0.0615	0.3790	-0.4520	0.1372	726 ± 55	661 ± 94	684 ± 55	486 ± 92
218839_at HEY1	hair/enhancer-of-split related with YRPW motif 1	-0.0202	0.0071	0.3356	0.2379	0.0046	1929 ± 123	1788 ± 140	1779 ± 167	1217 ± 52
218306_s_at HINT1	histidine triad nucleotide binding protein 1	-0.0280	0.0832	-0.4160	0.4486	0.3137	454 ± 48	424 ± 43	385 ± 32	348 ± 39
218946_at HIRIP5	HIRA interacting protein 5	-0.0055	0.0931	-0.0585	-0.2397	0.1480	1209 ± 202	1093 ± 192	949 ± 112	649 ± 142
208729_x_at HLA-B	major histocompatibility complex, class I, B	-0.0485	0.1848	-0.0247	0.2852	0.1475	1182 ± 209	823 ± 174	1040 ± 189	580 ± 158
211529_x_at HLA-G	HLA-G histocompatibility antigen, class I, G	-0.0392	0.1617	0.4775	-0.1772	0.4909	623 ± 55	614 ± 37	595 ± 43	520 ± 59
218152_at HMG20A	high-mobility group 20A	-0.0001	0.0021	-0.0204	0.2548	0.0470	2390 ± 334	2006 ± 222	1694 ± 160	1348 ± 172
200093_s_at HMGE	GrpE-like protein cochaperone	-0.0009	0.0001	-0.4224	-0.2795	0.0095	548 ± 25	486 ± 57	400 ± 41	333 ± 56
212434_at HMGN4	high mobility group nucleosomal binding domain 4	-0.0328	0.1576	-0.0548	-0.2072	0.0372	2259 ± 234	1908 ± 231	2192 ± 149	1408 ± 137
212676_x_at HNRPC	heterogeneous nuclear ribonucleoprotein C	-0.0404	0.0126	0.1915	-0.4326	0.0002	1078 ± 39	1052 ± 68	935 ± 35	741 ± 29
202579_x_at HNRPD	heterogeneous nuclear ribonucleoprotein D	-0.0248	0.0076	0.3495	-0.3117	0.0614	540 ± 80	528 ± 42	411 ± 32	332 ± 26
203330_s_at HNRPL	heterogeneous nuclear ribonucleoprotein L-like	-0.0418	0.0078	0.1833	-0.1610	0.0231	1361 ± 155	1401 ± 193	1067 ± 121	755 ± 54
209067_s_at HNRPK	heterogeneous nuclear ribonucleoprotein K	-0.0418	0.0076	0.1833	-0.1610	0.0231	1361 ± 155	1401 ± 193	1067 ± 121	755 ± 54
208766_s_at HNRPR	heterogeneous nuclear ribonucleoprotein R	-0.0364	0.1974	-0.1714	0.3809	0.3686	2330 ± 131	2401 ± 73	2127 ± 92	2105 ± 202
200097_s_at HPCA	hippocalcin	-0.0275	0.0232	0.2932	0.0725	0.0874	1828 ± 167	1974 ± 257	1650 ± 128	1260 ± 160
219671_at HPCAL4	hippocalcin like 4	-0.0541	0.0247	-0.3544	0.1130	0.0315	1789 ± 211	1136 ± 179	1463 ± 196	994 ± 153
205454_at HPRT1	hypoxanthine phosphoribosyltransferase 1	-0.0190	0.0017	-0.4129	0.2393	0.1540	5236 ± 932	4404 ± 1192	2761 ± 479	2990 ± 610
202854_at HRI	heme-regulated initiation factor 2-α kinase	-0.0033	0.0422	-0.4344	-0.0586	0.0108	1908 ± 362	1344 ± 202	1012 ± 156	620 ± 101
217736_s_at HRMT1L2	HMT1 hnRNP methyltransferase-like 2	-0.0371	0.0462	-0.1269	-0.3178	0.0001	2116 ± 111	2547 ± 55	1731 ± 75	1969 ± 113

Web Table 5 (52)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
206445_s_at	HS3ST2	heparan sulfate 3-O-sulfotransferase 2	-0.0063	0.0027	0.2747	0.1676	0.1883	1529 ± 115	1516 ± 170	1273 ± 33	1194 ± 159
218697_at	HSA243396	voltage-gated sodium channel β-3 subunit	-0.0155	0.0099	0.4324	0.1425	0.0346	1043 ± 105	945 ± 86	792 ± 95	649 ± 83
204405_x_at	HSA9761	putative dimethyladenosine transferase	-0.0189	0.3875	-0.4826	-0.0860	0.2417	874 ± 39	858 ± 50	883 ± 29	753 ± 70
218608_at	HSA9947	putative ATPase	-0.6319	0.0398	0.3550	0.3491	0.2830	929 ± 85	943 ± 109	877 ± 113	678 ± 99
217669_at	HSD17B12	hydroxysteroid dehydrogenase 12	-0.0439	0.7493	-0.3927	0.3385	0.6994	1847 ± 107	1619 ± 199	1624 ± 116	1700 ± 113
209657_s_at	HSF2	heat shock transcription factor 2	-0.0239	0.2089	0.4017	-0.0727	0.2622	275 ± 11	307 ± 42	258 ± 14	230 ± 33
204723_at	HSKM-B	HSKM-B protein	-0.0202	0.0077	0.2978	0.3616	0.0337	3718 ± 631	2296 ± 225	2073 ± 276	1984 ± 242
208744_x_at	HSP105B	heat shock 105KD	-0.0012	0.0082	-0.0337	0.0777	0.0150	462 ± 55	309 ± 77	228 ± 37	220 ± 38
206976_s_at	HSPA5	heat shock 70kDa protein 5	-0.0018	0.0149	-0.0090	0.1392	0.0184	5310 ± 630	3838 ± 557	2990 ± 331	2767 ± 115
211936_at	HSPA8	heat shock 70kDa protein 8	-0.0218	0.0340	-0.0645	0.1923	0.0186	2203 ± 259	1540 ± 177	1408 ± 167	1183 ± 38
206887_x_at	HSPA9B	heat shock 70kDa protein 9B	-0.0044	0.0283	-0.2667	0.1426	0.1074	3821 ± 653	2452 ± 466	2597 ± 396	2005 ± 444
208691_s_at	HSPC003	HSPC003 protein	-0.0072	0.0030	-0.0466	0.2915	0.1030	1920 ± 102	1834 ± 86	1657 ± 78	1578 ± 41
218026_at	HSPC009	HSPC009 protein	-0.0461	0.0521	0.2627	-0.3230	0.1358	2261 ± 60	2363 ± 282	2200 ± 117	1811 ± 51
218291_at	HSPC051	ubiquinol-cytochrome c reductase complex	-0.0101	0.0046	-0.4183	0.2948	0.0218	422 ± 16	406 ± 48	378 ± 35	284 ± 21
221570_s_at	HSPC133	HSPC133 protein	-0.0390	0.0792	-0.2256	0.4812	0.1497	874 ± 70	782 ± 80	636 ± 80	674 ± 97
218190_s_at	HSPC144	HSPC144 protein	-0.0281	0.0071	-0.4421	-0.4124	0.0283	6097 ± 570	6171 ± 548	4410 ± 394	4286 ± 643
218491_s_at	HSPC171	HSPC171 protein	-0.0004	0.0000	-0.3992	0.1759	0.0413	989 ± 63	1049 ± 44	855 ± 54	741 ± 117
211968_s_at	HSPCA	heat shock 90kDa protein 1, alpha	-0.0382	0.1059	-0.0100	0.1738	0.1110	4154 ± 682	2608 ± 460	3120 ± 537	2216 ± 401
200064_at	HSPCB	heat shock 90kDa protein 1, beta	-0.0009	0.0018	-0.0232	0.0583	0.0042	8350 ± 770	5982 ± 745	5472 ± 549	4407 ± 725
200806_s_at	HSPD1	heat shock 60kDa protein 1	-0.0402	0.0995	-0.0793	-0.3346	0.1567	852 ± 128	675 ± 131	701 ± 67	475 ± 68
214359_s_at	HSPF1	heat shock 10kDa protein 1	-0.0001	0.0105	-0.0529	-0.4753	0.0889	2432 ± 468	1818 ± 373	1593 ± 223	942 ± 393
204521_at	HSU79274	protein predicted by clone 23733	-0.0387	0.0532	-0.3176	-0.2337	0.1279	783 ± 67	699 ± 80	594 ± 32	587 ± 67
221622_s_at	HT007	uncharacterized hypothalamus protein HT007	-0.0187	0.2901	-0.1958	-0.3127	0.2623	1619 ± 117	1583 ± 184	1251 ± 118	1417 ± 159
205133_s_at	HT010	uncharacterized hypothalamus protein HT010	-0.0012	0.0085	-0.1683	0.2496	0.0188	887 ± 40	834 ± 73	708 ± 44	631 ± 67
201595_s_at	HT012	uncharacterized hypothalamus protein HT012	-0.0020	0.0087	-0.3344	-0.2897	0.0099	1367 ± 109	1118 ± 133	973 ± 56	842 ± 123
204555_at	HT021	HT021	-0.0020	0.0010	-0.2409	0.1205	0.0114	685 ± 40	744 ± 51	524 ± 53	543 ± 59
219288_at	HTR1E	5-hydroxytryptamine receptor 1E	-0.0346	0.0483	-0.3616	-0.1653	0.0053	1391 ± 111	1120 ± 96	1007 ± 62	903 ± 93
207135_at	HTR2A	5-hydroxytryptamine receptor 2A	-0.0763	0.0076	0.2894	0.4294	0.0662	955 ± 188	869 ± 142	633 ± 44	464 ± 66
207404_s_at	HYOU1	hypoxia up-regulated 1	-0.0485	0.0083	0.4628	0.0563	0.0346	159 ± 31	165 ± 29	80 ± 10	85 ± 18
200825_s_at	IARS	isoleucine-tRNA synthetase	-0.0057	0.0135	0.4911	0.3321	0.1428	3543 ± 82	3708 ± 359	3273 ± 264	2947 ± 126
210418_s_at	IDH3B	isocitrate dehydrogenase 3 β	-0.0194	0.0505	-0.3092	-0.1913	0.1327	678 ± 69	744 ± 128	574 ± 53	461 ± 55
206342_x_at	IDS	iduronate 2-sulfatase	-0.0071	0.0243	-0.1804	0.1371	0.0975	771 ± 86	757 ± 103	670 ± 47	510 ± 55
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	-0.1041	0.0316	-0.1982	-0.4728	0.0451	630 ± 73	636 ± 36	476 ± 68	352 ± 95
202439_s_at	IFNGR2	interferon γ receptor 2	-0.0021	0.0006	-0.2939	0.0865	0.3498	999 ± 53	989 ± 162	878 ± 91	765 ± 75
201642_at	IFRD1	interferon-related developmental regulator 1	-0.0005	0.0040	-0.0768	0.2327	0.0124	1607 ± 83	1491 ± 26	1404 ± 66	1291 ± 42
202147_s_at	IGF1	insulin-like growth factor 1	-0.0121	0.0056	0.2550	0.1383	0.0093	271 ± 31	235 ± 25	216 ± 28	116 ± 27
209541_at	ILF3	interleukin enhancer binding factor 3, 90kDa	-0.0322	0.0104	-0.3300	-0.2736	0.1265	191 ± 16	186 ± 16	152 ± 14	140 ± 23
200084_at	IMAGE145052	small acidic protein	-0.0305	0.0878	0.4675	-0.3261	0.2146	2933 ± 219	2958 ± 284	2738 ± 245	2230 ± 302
217805_at	INA	internexin neuronal intermediate filament protein, α	-0.0173	0.0027	-0.3045	0.4752	0.0016	500 ± 38	502 ± 28	510 ± 18	340 ± 20

Web Table 5 (53)

Probe set Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
214787_at	c-myc promoter-binding protein	-0.0709	0.0048	-0.0217	0.1709	0.0004	214 ± 13	177 ± 9	207 ± 7	134 ± 15
210213_s_at	integrin β 4 binding protein	-0.0357	0.1221	-0.1010	-0.3136	0.1684	498 ± 19	480 ± 61	469 ± 36	372 ± 30
217732_s_at	integral membrane protein 2B	-0.0143	0.1480	-0.3062	-0.3015	0.3425	7753 ± 278	8144 ± 340	6804 ± 759	6473 ± 4132
205874_at	Inositol 1,4,5-trisphosphate 3-kinase A	-0.2895	0.0031	0.2679	0.2537	0.0842	363 ± 43	339 ± 46	290 ± 41	208 ± 41
204465_s_at	inositol 1,4,5-trisphosphate receptor, type 1	-0.0144	0.0006	0.1510	0.4609	0.0086	2274 ± 293	2067 ± 333	1214 ± 134	1265 ± 119
209898_x_at	intersectin 2	-0.0950	0.0147	-0.4033	-0.2382	0.0492	1119 ± 96	1021 ± 84	1008 ± 59	797 ± 46
205842_s_at	Janus kinase 2	-0.4355	0.0469	0.4782	-0.4874	0.1167	108 ± 10	123 ± 11	121 ± 12	83 ± 15
211323_s_at	J domain containing protein 1	-0.0098	0.0472	-0.1619	-0.2128	0.1661	187 ± 37	203 ± 50	114 ± 18	100 ± 39
203456_at	JM4 protein	-0.0127	0.1020	-0.1452	0.1227	0.2817	840 ± 50	776 ± 80	668 ± 40	712 ± 91
218976_at	junctophilin 3	-0.0270	0.0459	-0.2447	0.3642	0.2171	1613 ± 64	1600 ± 285	1316 ± 126	1154 ± 90
220188_at	Kallmann syndrome 1 sequence	-0.0210	0.0080	-0.3868	0.1673	0.0710	243 ± 32	184 ± 43	138 ± 25	116 ± 35
203162_s_at	katalin p80 subunit B 1	-0.0638	0.0477	0.2589	0.0540	0.4090	1834 ± 283	1631 ± 225	1405 ± 107	1363 ± 220
210078_s_at	K ⁺ channel, shaker-related subfamily, β member 1	-0.0360	0.0088	0.2890	0.1088	0.0519	1426 ± 219	1429 ± 270	894 ± 104	752 ± 188
203402_at	K ⁺ channel, shaker-related subfamily, β member 2	-0.1121	0.0059	-0.4954	0.0568	0.0206	1702 ± 110	1719 ± 263	1793 ± 187	1061 ± 65
210471_s_at	K ⁺ channel, Shal-related subfamily, member 2	-0.0120	0.0015	0.4633	0.2535	0.0206	1031 ± 256	612 ± 125	315 ± 19	332 ± 63
210263_at	potassium voltage-gated channel, subfamily F, member 1	-0.2113	0.0157	0.1906	0.2435	0.1031	302 ± 39	284 ± 37	273 ± 47	165 ± 33
207103_at	Kv channel interacting protein 1	-0.0303	0.0362	-0.2481	0.0262	0.0063	599 ± 77	477 ± 67	334 ± 41	301 ± 50
221307_at	K ⁺ inwardly-rectifying channel, subfamily J, member 3	-0.0206	0.0139	0.1317	0.1823	0.1303	255 ± 18	209 ± 25	201 ± 15	174 ± 38
204679_at	potassium channel, subfamily K, member 1	-0.0952	0.0487	-0.4763	0.3852	0.4129	1263 ± 134	1316 ± 50	1146 ± 108	1007 ± 178
207142_at	intermediate/small g Ca ⁺⁺ activated K ⁺ channel, N2	-0.0253	0.0061	0.2089	0.3596	0.0989	137 ± 26	136 ± 20	91 ± 13	72 ± 18
205737_at	K ⁺ voltage-gated channel, KQT-like subfamily, member 2	-0.0579	0.0165	-0.3753	0.0906	0.1774	3002 ± 309	2645 ± 404	2203 ± 305	2083 ± 214
200699_at	KDEL endoplasmic reticulum protein retention receptor 2	-0.0349	0.1439	-0.1632	0.3752	0.2144	573 ± 46	557 ± 34	553 ± 93	395 ± 37
202753_at	26S proteasome non-ATPase regulatory subunit	-0.0121	0.0856	-0.2772	0.2780	0.0835	1356 ± 110	1281 ± 137	961 ± 82	1106 ± 136
212215_at	putative L-type neutral amino acid transporter	-0.0731	0.0432	-0.2785	-0.3937	0.0468	4121 ± 362	3701 ± 464	4198 ± 214	2676 ± 481
200040_at	KIAA0749 protein/ Dendrin	-0.0081	0.0028	0.4395	0.0182	0.0563	1524 ± 161	1641 ± 190	1178 ± 120	1093 ± 50
214788_x_at	yeast Sec31p homolog	-0.0008	0.0080	-0.0137	-0.2660	0.0565	3347 ± 309	3178 ± 591	2570 ± 333	1852 ± 351
200945_s_at	tomosyn-like	-0.0132	0.0047	-0.3342	-0.2212	0.0108	2166 ± 81	1972 ± 97	1952 ± 102	1608 ± 156
215518_at	homolog of rat kinase D-interacting substance of 220 kDa	-0.0015	0.0020	-0.0208	0.0694	0.0480	605 ± 42	628 ± 57	525 ± 44	446 ± 44
209234_at	kinesin family member 1B	-0.0038	0.1867	-0.0227	0.2863	0.4746	5189 ± 229	4970 ± 315	4743 ± 209	4688 ± 277
203087_s_at	kinesin heavy chain member 2	-0.0631	0.0365	0.4930	-0.2882	0.0784	710 ± 34	698 ± 73	600 ± 22	538 ± 62
212163_at	kinesin family member 3C	-0.0261	0.0233	0.4004	0.3889	0.0088	2276 ± 58	2107 ± 68	1908 ± 62	1841 ± 238
203130_s_at	kinesin family member 5C	-0.0446	0.1471	-0.0291	0.4904	0.4423	9415 ± 336	8693 ± 827	8447 ± 608	8112 ± 467
203389_at	kinesin-associated protein 3	-0.0286	0.0237	-0.4724	0.1346	0.0436	2242 ± 292	1719 ± 177	1508 ± 161	1426 ± 151
203333_at	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	-0.0155	0.0191	-0.4195	0.1154	0.1020	1100 ± 182	856 ± 128	669 ± 68	637 ± 162
205051_s_at	klotho	-0.0041	0.0027	0.2804	0.3225	0.0200	1882 ± 310	1350 ± 286	778 ± 44	1034 ± 200
212877_at	kinesin 2 60/70kDa	-0.0828	0.0204	-0.3794	0.1587	0.1179	2289 ± 394	1697 ± 330	1382 ± 231	1219 ± 328
201088_at	karyopherin α 2	-0.0066	0.0081	-0.1845	-0.4971	0.0015	2522 ± 177	2093 ± 197	1668 ± 155	1585 ± 143
211762_s_at	karyopherin α 3	-0.0080	0.0057	-0.2107	0.3263	0.0223	828 ± 61	695 ± 98	529 ± 35	522 ± 93
211952_at	karyopherin β 3	-0.0139	0.1522	-0.1459	0.2778	0.1613	520 ± 25	428 ± 29	467 ± 50	395 ± 52

Web Table 5 (54)

Probe set Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
208975_s_at L1CAM	L1 cell adhesion molecule	-0.0132	0.0031	-0.4496	0.3078	0.0382	506 ± 21	527 ± 69	404 ± 16	365 ± 40
204584_at LAGY	lung cancer-associated Y protein	-0.0373	0.0373	-0.3482	0.2040	0.0145	1150 ± 186	1054 ± 148	613 ± 53	597 ± 40
202020_s_at LANCL1	LanC lantibiotic synthetase component C-like 1	-0.0101	0.1951	-0.3821	0.4683	0.5044	4720 ± 276	4653 ± 622	4430 ± 364	3857 ± 465
211597_s_at LARGE	like-glycosyltransferase	-0.0129	0.0060	0.2778	0.1769	0.1144	2302 ± 194	1797 ± 154	1639 ± 221	1573 ± 132
214039_s_at LC27	putative integral membrane transporter	-0.0154	0.4047	0.2847	-0.1397	0.5371	2458 ± 147	2600 ± 289	2326 ± 93	2187 ± 121
215543_s_at LDB2	LIM domain binding 2	-0.0087	0.0010	-0.3993	0.1717	0.0571	1140 ± 101	1081 ± 158	834 ± 66	770 ± 87
206481_s_at LDHA	lactate dehydrogenase A	-0.0002	0.0015	-0.0827	-0.3715	0.0074	1740 ± 347	1243 ± 204	796 ± 104	560 ± 95
204454_at LDOC1	leucine zipper, down-regulated in cancer 1	-0.0214	0.0792	-0.3766	0.3726	0.1781	2494 ± 326	2308 ± 440	1660 ± 111	1850 ± 203
200650_s_at LEC3	KIAA0768 protein	-0.0092	0.0320	-0.4322	0.3628	0.0054	5673 ± 285	4997 ± 758	4079 ± 292	3184 ± 540
203619_s_at LFG	lifeguard	-0.0021	0.0067	-0.0271	-0.4897	0.0416	2634 ± 203	2468 ± 295	2140 ± 163	1807 ± 135
208938_x_at LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	0.0000	0.0033	-0.0256	-0.3466	0.0073	532 ± 12	528 ± 40	388 ± 35	379 ± 57
211219_s_at LHX2	LIM homeobox protein 2	-0.0293	0.0822	0.4641	0.2976	0.3964	464 ± 31	451 ± 23	369 ± 59	373 ± 66
208934_s_at LMO4	LIM domain only 4	-0.0102	0.0088	0.4526	0.1155	0.0242	354 ± 37	301 ± 36	222 ± 27	201 ± 49
213510_x_at LOC220594	TL132 protein	-0.0384	0.5947	0.2075	-0.0214	0.6152	2490 ± 121	2565 ± 153	2429 ± 226	2220 ± 111
208205_s_at LOC51001	CGI-12 protein	-0.0432	0.0057	0.3782	-0.1588	0.0324	3592 ± 560	2627 ± 498	1970 ± 239	1845 ± 87
218628_at LOC51019	CGI-116 protein	-0.0328	0.5029	-0.2642	-0.0944	0.5482	408 ± 25	434 ± 72	436 ± 27	338 ± 73
218193_s_at LOC51026	CGI-141 protein	-0.0662	0.0287	-0.3640	0.4606	0.0793	254 ± 17	239 ± 21	214 ± 22	169 ± 31
219363_s_at LOC51031	CGI-150 protein	-0.0019	0.0013	0.4726	-0.4585	0.0060	416 ± 17	431 ± 12	384 ± 25	318 ± 26
219055_s_at LOC51072	C21orf19-like protein	-0.0034	0.7906	-0.1375	-0.3174	0.7946	708 ± 20	670 ± 53	657 ± 27	652 ± 67
209092_s_at LOC51094	CGI-45 protein	-0.0073	0.0070	0.1319	0.2019	0.0026	738 ± 55	652 ± 72	571 ± 64	369 ± 42
203721_s_at LOC51096	CGI-48 protein	-0.0007	0.1188	-0.1623	0.0444	0.1178	783 ± 50	697 ± 16	621 ± 19	667 ± 83
201825_s_at LOC51097	CGI-49 protein	-0.0471	0.2583	-0.3802	-0.2278	0.0524	488 ± 40	484 ± 53	320 ± 31	417 ± 64
217748_at LOC51102	CGI-63 protein	-0.0424	0.0340	0.4373	-0.0725	0.0130	1141 ± 45	1214 ± 78	994 ± 28	985 ± 51
218059_at LOC51123	HSPC038 protein	-0.0401	0.4048	0.0097	-0.0067	0.0004	1544 ± 49	1855 ± 57	1203 ± 79	1552 ± 126
217720_at LOC51142	16.7Kd protein	-0.0285	0.0969	-0.4313	0.1931	0.1023	5411 ± 491	4552 ± 626	3525 ± 209	4180 ± 696
218664_at LOC51182	likely ortholog of mouse heat shock protein, 70 kDa 4	-0.0135	0.0156	0.4148	0.4646	0.0255	237 ± 18	283 ± 17	244 ± 20	146 ± 49
218671_s_at LOC51189	ATPase inhibitor precursor	-0.0214	0.0607	0.4905	-0.2050	0.3419	903 ± 86	923 ± 113	798 ± 79	682 ± 121
218657_at LOC51195	Link guanidine nucleotide exchange factor II	-0.1778	0.0184	-0.0451	0.0488	0.0305	760 ± 53	459 ± 72	633 ± 128	377 ± 110
219212_at LOC51202	hsp0256 protein	-0.0317	0.0224	-0.0907	0.2725	0.1240	294 ± 42	260 ± 45	185 ± 31	168 ± 50
221069_s_at LOC51204	clone HQ0477 PRO0477p	-0.5506	0.0201	-0.4025	0.1120	0.2245	362 ± 30	334 ± 11	311 ± 25	290 ± 26
218915_at LOC51219	clone FLB5214	-0.0481	0.0815	-0.1092	0.1043	0.3074	1333 ± 145	1144 ± 122	1190 ± 31	1036 ± 86
220890_s_at LOC51290	CDA14	-0.0166	0.0362	-0.2420	-0.2503	0.0973	917 ± 34	821 ± 77	812 ± 45	720 ± 60
217990_at LOC51292	GMPR2 for guanosine monophosphate reductase isolog	-0.0575	0.0338	0.0754	-0.0959	0.0894	640 ± 20	636 ± 60	584 ± 21	487 ± 67
205331_s_at LOC51308	SGC32445 protein	-0.1475	0.0292	0.4047	0.2224	0.1718	721 ± 52	796 ± 91	743 ± 76	573 ± 49
219872_at LOC51313	AD021 protein	-0.4511	0.0442	0.1116	0.1389	0.2708	93 ± 14	85 ± 15	80 ± 19	49 ± 16
221488_s_at LOC51596	divalent cation tolerant protein CUTA	-0.0174	0.1974	0.3259	0.3374	0.2527	3518 ± 253	3562 ± 235	2957 ± 75	3196 ± 292
218135_at LOC51622	CGI-43 protein	-0.0061	0.0187	0.3293	-0.1997	0.0999	548 ± 29	510 ± 46	484 ± 20	420 ± 47
203763_at LOC51626	CGI-60 protein	-0.1172	0.0009	0.0572	-0.3188	0.0179	437 ± 36	462 ± 43	377 ± 41	280 ± 35
218732_at LOC51651	CGI-147 protein	-0.0060	0.1236	0.0673	-0.3140	0.0950	419 ± 27	458 ± 6	340 ± 32	343 ± 60

Web Table 5 (55)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
215891_x_at	LOC51668	HSPCO34 protein	-0.1426	0.0099	0.4755	0.1328	0.0148	1060 ± 77	878 ± 36	916 ± 40	782 ± 30
201973_s_at	LOC51714	selanoprotein T	-0.0416	0.0150	-0.2863	0.0971	0.0446	2750 ± 146	2793 ± 181	2536 ± 108	2178 ± 188
220046_s_at	LOC57018	cyclin L anla-6a	-0.0174	0.5403	-0.0028	0.4446	0.1491	851 ± 54	707 ± 32	702 ± 33	755 ± 78
217811_at	LOC57406	lipase protein	-0.0366	0.0094	-0.2472	-0.4963	0.0779	1080 ± 125	956 ± 95	736 ± 96	694 ± 142
45288_at	LOC81034	folate transporter/carrier	-0.0287	0.0117	0.1829	0.1629	0.0178	1012 ± 41	915 ± 40	867 ± 37	805 ± 55
221020_s_at	LPHH1	latrophilin 1	-0.0162	0.0047	-0.4168	0.2421	0.0596	450 ± 62	369 ± 17	342 ± 9	276 ± 44
206553_s_at	LRP1B	low density lipoprotein-related protein 1B	-0.0127	0.0020	0.0665	-0.3828	0.0322	387 ± 42	327 ± 44	306 ± 21	213 ± 42
219843_at	LRP8	low density lipoprotein receptor	-0.0047	0.0216	0.2200	-0.3432	0.0119	685 ± 73	705 ± 54	628 ± 62	404 ± 53
211971_s_at	LRPPRC	leucine-rich PPR-motif containing	-0.0824	0.0081	0.4138	0.3324	0.0602	982 ± 112	1016 ± 109	845 ± 21	668 ± 54
209840_s_at	LRRN3	leucine-rich repeat protein, neuronal 3	-0.0560	0.0405	0.3458	-0.0574	0.0842	461 ± 37	507 ± 57	461 ± 33	343 ± 46
205282_at	LSM3	Lsm3 protein	-0.0340	0.0214	-0.4762	0.2861	0.0920	476 ± 41	481 ± 48	421 ± 28	342 ± 48
202736_s_at	LSM4	U6 snRNA-associated Sm-like protein	-0.0249	0.1251	-0.4933	-0.4034	0.2614	415 ± 35	469 ± 21	382 ± 27	344 ± 76
218729_at	LXN	latexin protein	-0.0165	0.1529	-0.4764	0.3223	0.1136	139 ± 20	111 ± 15	65 ± 16	94 ± 33
202504_s_at	LZTS1	leucine zipper, putative tumor suppressor 1	-0.0187	0.0002	-0.2231	0.1074	0.0151	92 ± 9	95 ± 9	93 ± 7	59 ± 6
47550_at	M9	muscle specific gene	-0.0046	0.0021	0.2507	-0.4562	0.0242	558 ± 38	504 ± 56	462 ± 47	359 ± 30
221494_x_at	MAGED1	melanoma antigen, family D, 1	-0.0160	0.0095	0.2801	0.3368	0.0501	2060 ± 141	1816 ± 197	1684 ± 138	1446 ± 56
219894_at	MAGEL2	MAGE-like 2	-0.1227	0.0232	0.4401	0.0626	0.3472	260 ± 29	219 ± 17	203 ± 36	186 ± 32
209014_at	MAO1A	mannosidase, α, class 1A, member 1	-0.0033	0.0015	0.2771	0.4525	0.0369	3178 ± 433	2993 ± 317	2108 ± 176	2053 ± 181
212741_at	MAO1A	mannosidase, α, class 1A, member 1	-0.0251	0.0034	-0.0281	0.0459	0.0089	1111 ± 134	1039 ± 197	703 ± 68	531 ± 73
212741_at	MAP-1	modulator of apoptosis 1	-0.0452	0.0185	-0.4700	0.1163	0.0208	1373 ± 102	1190 ± 59	1159 ± 76	993 ± 58
203151_at	MAP1A	microtubule-associated protein 1A	-0.2343	0.0081	-0.3772	0.1957	0.0963	11713 ± 600	1413 ± 1101	1388 ± 1115	8799 ± 488
202670_at	MAP2K1	mitogen-activated protein kinase kinase 1	-0.0653	0.0425	-0.4379	0.0944	0.1021	2563 ± 551	1749 ± 385	1204 ± 88	1449 ± 403
217971_at	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	-0.1034	0.0370	-0.2423	0.3544	0.1706	586 ± 30	599 ± 25	518 ± 32	484 ± 63
212508_at	MAP2K4	mitogen-activated protein kinase kinase 4	-0.0403	0.0202	-0.0292	0.1064	0.0272	3675 ± 630	2771 ± 366	1647 ± 146	2163 ± 459
218311_at	MAP4K3	mitogen-activated protein kinase kinase 3	-0.0286	0.1537	0.2173	-0.4260	0.3954	587 ± 58	562 ± 64	479 ± 38	479 ± 62
204813_at	MAPK10	mitogen-activated protein kinase kinase 10	-0.0432	0.1331	0.2602	0.4829	0.3283	2161 ± 145	2139 ± 175	1800 ± 144	1930 ± 184
202530_at	MAPK14	mitogen-activated protein kinase 14	-0.1179	0.0099	0.4739	0.1149	0.1209	508 ± 23	480 ± 42	468 ± 29	401 ± 17
213014_at	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	-0.0340	0.2862	0.2459	0.0680	0.4696	217 ± 31	189 ± 16	158 ± 12	187 ± 34
203266_s_at	MAPK9	mitogen-activated protein kinase 9	-0.0172	0.0071	-0.4511	-0.4046	0.0378	1519 ± 123	1249 ± 198	936 ± 93	1072 ± 171
203218_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	-0.0439	0.0247	-0.3259	0.2509	0.0858	805 ± 82	747 ± 87	645 ± 44	536 ± 84
203841_x_at	MARS	methionine-tRNA synthetase	0.0000	0.0001	-0.0004	0.1363	0.0948	269 ± 50	205 ± 61	132 ± 29	117 ± 44
201475_x_at	MASA	E-1 enzyme	-0.0446	0.0036	0.3505	0.2150	0.0000	1803 ± 60	1457 ± 118	1293 ± 46	1100 ± 71
206267_s_at	MATK	megakaryocyte-associated tyrosine kinase	-0.0206	0.1345	-0.3783	-0.2390	0.2885	272 ± 30	307 ± 49	284 ± 41	195 ± 42
206226_s_at	MATR3	matrin 3	-0.0676	0.0097	-0.2578	0.2684	0.0855	4287 ± 485	4195 ± 251	3500 ± 364	2701 ± 604
218440_at	MCCC1	methylcrotonyl-Coenzyme A carboxylase 1	-0.0475	0.2399	0.2557	-0.3499	0.2535	569 ± 36	614 ± 34	565 ± 47	499 ± 26
209623_at	MCCC2	methylcrotonyl-Coenzyme A carboxylase 2	-0.0180	0.1887	0.3108	0.3034	0.3790	912 ± 55	895 ± 27	754 ± 53	812 ± 129
217956_s_at	MCM4	MCM4 minichromosome maintenance deficient 4	-0.0234	0.0007	0.0920	0.3833	0.0204	1996 ± 152	2047 ± 77	1881 ± 36	1455 ± 177
218163_at	MCT-1	MCT-1 protein	-0.0418	0.0853	-0.4930	0.3843	0.1596	567 ± 87	495 ± 97	338 ± 38	378 ± 84
222036_s_at	MDH1	malate dehydrogenase 1, NAD	-0.0130	0.0129	0.4999	0.2440	0.0106	222 ± 24	248 ± 14	186 ± 15	151 ± 20

Web Table 5 (56)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
200978_at	malate dehydrogenase 2, NAD	-0.0226	0.0067	-0.4993	0.2123	0.0694	6822 ± 1292	5583 ± 1159	3397 ± 658	3337 ± 1012
218877_s_at	MDS024 protein	-0.0081	0.0959	0.3106	0.4829	0.3173	410 ± 43	399 ± 48	339 ± 33	304 ± 56
204059_s_at	malic enzyme 1, NADP-dependent, cytosolic	-0.2868	0.0186	0.3213	0.2996	0.2666	699 ± 32	692 ± 20	671 ± 50	585 ± 61
204663_at	malic enzyme 3, NADP-dependent, mitochondrial	-0.1852	0.0115	0.1769	0.2631	0.1509	510 ± 77	522 ± 56	417 ± 42	342 ± 12
207079_s_at	RNA polymerase II transcriptional regulation mediator	-0.0332	0.5551	-0.3561	-0.2726	0.7401	269 ± 15	266 ± 32	253 ± 26	227 ± 43
212535_at	MADS box transcription enhancer factor 2, polypeptide A	-0.0192	0.6612	-0.0416	-0.2256	0.4413	1536 ± 46	1513 ± 128	1675 ± 133	1375 ± 181
209199_s_at	MADS box transcription enhancer factor 2, polypeptide C	-0.0450	0.2145	-0.2858	-0.0316	0.2992	668 ± 59	749 ± 83	625 ± 62	567 ± 58
212732_at	maternally expressed 3	-0.1756	0.0205	-0.3999	0.3011	0.2164	1063 ± 73	1062 ± 123	1031 ± 128	781 ± 83
212673_at	methionyl aminopeptidase 1	-0.0418	0.1857	0.2926	0.2774	0.3786	946 ± 66	877 ± 51	822 ± 41	826 ± 66
207098_s_at	mitofusin 1	-0.0023	0.0168	-0.0349	-0.2853	0.0226	247 ± 13	248 ± 20	238 ± 17	175 ± 20
212945_s_at	MAX dimerization protein 5	-0.0095	0.0143	-0.0216	0.4838	0.0362	254 ± 36	219 ± 15	225 ± 36	111 ± 27
200899_s_at	meningioma expressed antigen 5	-0.0275	0.7519	-0.2568	0.1994	0.8733	2114 ± 128	1937 ± 176	1989 ± 173	1954 ± 187
203545_at	monoglyceride lipase	-0.0177	0.0033	-0.1921	0.0069	0.0000	701 ± 15	636 ± 19	517 ± 19	569 ± 18
211026_s_at	microsomal glutathione S-transferase 3	-0.0015	0.0080	-0.3895	0.4265	0.0667	2671 ± 109	2619 ± 222	2221 ± 173	2142 ± 33
209209_s_at	mitogen inducible 2	-0.0057	0.0745	-0.3279	-0.3744	0.1408	304 ± 38	266 ± 59	190 ± 25	190 ± 29
201403_s_at	McKusick-Kaufman syndrome	-0.0137	0.0019	-0.0088	0.0224	0.0493	4095 ± 297	3818 ± 369	3422 ± 281	2804 ± 353
218138_at	myosin, light polypeptide, regulatory, non-sarcomeric	-0.0008	0.0034	0.2264	0.3450	0.0006	850 ± 26	662 ± 68	568 ± 29	589 ± 52
201318_s_at	myosin regulatory light chain	-0.0026	0.0101	0.4656	0.3700	0.0274	1451 ± 65	1399 ± 151	1156 ± 131	916 ± 172
200948_at	myeloid leukemia factor 2	-0.0239	0.0678	-0.2245	-0.1881	0.2238	2621 ± 195	2764 ± 300	2411 ± 169	2102 ± 229
212474_at	monocyte to macrophage differentiation-associated	-0.0223	0.0152	0.1860	0.2933	0.1091	4248 ± 449	4205 ± 714	3291 ± 379	2589 ± 574
204959_at	myeloid cell nuclear differentiation antigen	-0.0468	0.3856	0.0000	-0.0024	0.0823	90 ± 7	140 ± 19	104 ± 27	69 ± 15
203414_at	MO25 protein	-0.0466	0.0279	-0.4554	0.0713	0.0775	4073 ± 602	3966 ± 1019	2254 ± 250	2240 ± 430
218212_s_at	molybdenum cofactor synthesis 2	-0.0526	0.0175	-0.2544	0.3474	0.1032	691 ± 51	620 ± 84	582 ± 42	443 ± 99
209582_s_at	antigen identified by monoclonal antibody MRC OX-2	-0.0077	0.0063	-0.2712	0.2555	0.0115	309 ± 42	260 ± 25	204 ± 13	174 ± 18
209583_s_at	metalloprotease 1	-0.0089	0.0063	-0.0604	0.2531	0.0284	1448 ± 162	1191 ± 134	1053 ± 109	874 ± 85
205273_s_at	membrane protein, palmitoylated 1, 55kDa	-0.0035	0.0023	-0.1599	-0.4753	0.0917	891 ± 69	873 ± 72	724 ± 68	660 ± 84
202974_at	metallo phosphoesterase	-0.0366	0.0486	0.2817	-0.2191	0.0250	916 ± 68	890 ± 63	764 ± 38	623 ± 95
214071_at	MpV17 transgene, murine homolog, glomerulosclerosis	-0.0229	0.0117	-0.0429	0.3221	0.1863	314 ± 21	346 ± 44	296 ± 24	226 ± 56
218049_s_at	mitochondrial ribosomal protein L13	-0.0183	0.0815	0.3909	0.1454	0.4149	237 ± 15	216 ± 20	188 ± 15	181 ± 43
203466_at	mitochondrial ribosomal protein L15	-0.0029	0.0002	-0.0220	0.0269	0.0767	315 ± 46	286 ± 69	181 ± 51	136 ± 47
218027_at	mitochondrial ribosomal protein L16	-0.0022	0.0004	0.3348	0.1211	0.0001	692 ± 42	522 ± 42	394 ± 49	399 ± 32
217907_at	mitochondrial ribosomal protein L18	-0.0397	0.1117	0.4519	-0.4517	0.0485	1080 ± 49	1025 ± 68	850 ± 29	927 ± 89
203465_at	mitochondrial ribosomal protein L19	-0.2313	0.0268	-0.3700	0.2463	0.0643	172 ± 16	178 ± 24	188 ± 32	100 ± 18
217980_s_at	mitochondrial ribosomal protein L20	-0.0428	0.0046	0.2555	0.4913	0.0046	627 ± 42	555 ± 12	485 ± 55	402 ± 9
218339_at	mitochondrial ribosomal protein L22	-0.0332	0.8265	-0.0710	-0.2524	0.8795	375 ± 23	361 ± 38	361 ± 14	340 ± 44
220526_s_at	mitochondrial ribosomal protein L3	-0.0023	0.0030	-0.2427	0.2419	0.0349	1511 ± 153	1513 ± 43	1209 ± 109	1043 ± 127
218106_s_at	mitochondrial ribosomal protein S10	-0.0944	0.0169	0.0258	-0.4331	0.0617	709 ± 47	825 ± 50	681 ± 24	625 ± 67
221437_s_at	mitochondrial ribosomal protein S15	-0.3056	0.0267	-0.2717	0.2956	0.0923	206 ± 25	163 ± 30	120 ± 18	119 ± 38
219819_s_at	mitochondrial ribosomal protein S28	-0.0275	0.1570	0.3632	-0.1572	0.3578	389 ± 32	374 ± 62	302 ± 28	285 ± 64

Web Table 5 (57)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
209421_at	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1	-0.2981	0.0487	-0.4509	-0.4918	0.1766	255 ± 25	208 ± 29	197 ± 21	176 ± 29
217772_s_at	MTCH2	mitochondrial carrier homolog 2	-0.0203	0.6855	0.2472	0.4905	0.8003	592 ± 27	599 ± 53	536 ± 56	586 ± 63
208787_at	MTFHD1	methylentetrahydrofolate dehydrogenase	-0.0023	0.0002	0.0934	0.0856	0.0275	1304 ± 99	1199 ± 125	1024 ± 55	880 ± 114
216095_x_at	MTMR1	myotubularin related protein 1	-0.0096	0.1270	-0.2918	0.3099	0.3767	1334 ± 78	1252 ± 56	1249 ± 39	1151 ± 95
212277_at	MTMR4	myotubularin related protein 4	-0.0251	0.4555	-0.1919	0.3735	0.3577	893 ± 39	854 ± 43	759 ± 55	796 ± 91
213278_at	MTMR9	myotubularin related protein 9	-0.0762	0.0041	-0.4788	0.2304	0.0424	1222 ± 67	1093 ± 54	979 ± 74	969 ± 78
202309_at	MTX2	metaxin 2	-0.0054	0.0126	-0.1471	0.2275	0.0026	911 ± 76	868 ± 86	722 ± 34	554 ± 44
203517_at	my048	my048 protein	-0.0250	0.0019	-0.3111	0.3382	0.0269	651 ± 65	488 ± 78	438 ± 54	375 ± 58
211276_at	MYT1L	myelin transcription factor 1-like	-0.0012	0.0006	-0.1518	0.1210	0.0200	4285 ± 328	3738 ± 337	3392 ± 309	2771 ± 318
210016_at	NAP1L2	nucleosome assembly protein 1-like 2	-0.0200	0.0138	-0.2545	0.4071	0.0097	4307 ± 343	3359 ± 488	2698 ± 385	2224 ± 531
219369_at	NARS	asparaginyl-tRNA synthetase	-0.0071	0.0274	-0.2094	-0.4379	0.0370	2608 ± 419	1948 ± 373	1304 ± 172	1302 ± 348
201521_s_at	NCBP2	nuclear cap binding protein subunit 2, 20kDa	-0.4544	0.0299	-0.2954	0.3438	0.3870	186 ± 15	177 ± 22	165 ± 27	131 ± 28
200027_at	NDRG4	NDRG family member 4	-0.0088	0.0024	-0.4416	0.2773	0.0324	5969 ± 298	5177 ± 478	5037 ± 112	4550 ± 340
209159_s_at	NDUFA10	NADH dehydrogenase 1 α subcomplex, 10, 42kDa	-0.0050	0.0006	-0.0851	0.0636	0.0369	4100 ± 455	3612 ± 619	2957 ± 380	2038 ± 470
217860_at	NDUFA2	NADH dehydrogenase 1 α subcomplex, 2, 8kDa	-0.0434	0.0368	0.3786	-0.1656	0.0057	2018 ± 143	1727 ± 104	1598 ± 74	1384 ± 129
218563_at	NDUFA3	NADH dehydrogenase 1 α subcomplex, 3, 9kDa	-0.0545	0.0039	-0.4208	0.0993	0.0447	3350 ± 308	2820 ± 142	2831 ± 265	2282 ± 170
209224_s_at	NDUFA4	NADH dehydrogenase 1 α subcomplex, 4, 9kDa	-0.0036	0.0006	0.3884	0.2012	0.0767	1716 ± 111	1767 ± 170	1625 ± 99	1297 ± 134
217773_s_at	NDUFA5	NADH dehydrogenase 1 α subcomplex, 5, 13kDa	-0.0144	0.0013	0.4001	0.4492	0.0071	6163 ± 670	5522 ± 595	4688 ± 346	3212 ± 376
202785_at	NDUFA7	NADH dehydrogenase 1 α subcomplex, 7, 14.5kDa	-0.2010	0.0456	-0.3884	0.2929	0.1759	249 ± 37	207 ± 66	219 ± 38	105 ± 40
201304_at	NDUFA8	NADH dehydrogenase 1 α subcomplex, 8, 19kDa	-0.0071	0.0002	0.3567	0.1482	0.0095	2449 ± 361	2224 ± 321	1732 ± 161	988 ± 155
202077_at	NDUFAB1	NADH dehydrogenase 1 α subcomplex, 1, 8kDa	-0.0410	0.1346	-0.2825	-0.4230	0.2644	2399 ± 265	2293 ± 364	1626 ± 260	1837 ± 366
218160_at	NDUFB1	NADH dehydrogenase 1 β subcomplex, 1, 7kDa	-0.0060	0.0107	0.4807	-0.3705	0.0043	1703 ± 159	1552 ± 98	1284 ± 79	1073 ± 99
206790_s_at	NDUFB2	NADH dehydrogenase 1 β subcomplex, 2, 8kDa	-0.0081	0.0173	-0.2001	0.1919	0.0554	3317 ± 277	3188 ± 328	2827 ± 65	2319 ± 282
203371_s_at	NDUFB3	NADH dehydrogenase 1 β subcomplex, 3, 12kDa	-0.1416	0.0104	-0.0468	0.0024	0.0302	1218 ± 95	961 ± 31	1007 ± 66	877 ± 92
218200_s_at	NDUFB4	NADH dehydrogenase 1 β subcomplex, 4, 15kDa	-0.0237	0.0393	-0.1550	0.4898	0.0642	3210 ± 265	2755 ± 243	2524 ± 198	2284 ± 261
218226_s_at	NDUFB5	NADH dehydrogenase 1 β subcomplex, 5, 16kDa	-0.0197	0.0142	-0.4017	0.4832	0.0593	3537 ± 236	3153 ± 440	2255 ± 156	2471 ± 541
203621_at	NDUFB8	NADH dehydrogenase 1 β subcomplex, 8, 19kDa	-0.0026	0.0001	-0.0405	0.1912	0.1054	1380 ± 145	1304 ± 128	1092 ± 137	909 ± 137
218101_s_at	NDUFC2	NADH dehydrogenase 1, subcomplex unknown, 2, 14.5kDa	-0.0241	0.0889	0.4872	0.4107	0.2271	3256 ± 364	2834 ± 422	2387 ± 244	2325 ± 404
201226_at	NDUFS2	NADH dehydrogenase Fe-S protein 2, 49kDa	-0.0379	0.0221	-0.1945	0.0709	0.0007	2559 ± 119	2383 ± 192	2165 ± 199	1444 ± 95
201966_at	NDUFS3	NADH dehydrogenase Fe-S protein 3, 30kDa	-0.0469	0.0066	0.2873	0.3558	0.1620	1533 ± 101	1437 ± 125	1245 ± 63	1249 ± 138
201740_at	NDUFS4	NADH dehydrogenase Fe-S protein 4, 18kDa	-0.0299	0.0107	0.4564	0.1919	0.0721	1888 ± 202	1832 ± 172	1513 ± 128	1282 ± 174
209303_at	NDUFV2	NADH dehydrogenase flavoprotein 2, 24kDa	-0.0010	0.0002	0.4638	0.3367	0.0113	870 ± 127	679 ± 76	454 ± 25	502 ± 58
201840_at	NEDD8	neural precursor expressed, developmentally down-regulated 8	-0.0509	0.0349	-0.0109	0.2999	0.0880	1296 ± 78	1003 ± 166	1033 ± 79	817 ± 193
202941_at	NEF3	neurofilament 3	-0.0189	0.0007	0.3506	0.1201	0.0012	1319 ± 117	1252 ± 97	970 ± 63	753 ± 66
33767_at	NEFH	neurofilament, heavy polypeptide 200kDa	-0.1762	0.0214	-0.4405	0.0567	0.0786	2478 ± 444	1742 ± 392	2283 ± 617	817 ± 213
205113_at	NEFL	neurofilament, light polypeptide 68kDa	-0.0257	0.0041	0.4448	0.1919	0.0111	4061 ± 648	3177 ± 430	2827 ± 587	1320 ± 203
206089_at	NELL1	NEL-like 1	-0.0574	0.0067	-0.2908	0.0448	0.0042	285 ± 72	88 ± 20	72 ± 13	50 ± 10
221805_at	NELL2	NEL-like 2	-0.0234	0.0352	0.4124	0.2082	0.0383	4381 ± 1058	3055 ± 656	2244 ± 574	1184 ± 340
206949_s_at	NESCA	nesca protein	-0.1969	0.0457	-0.2894	0.3162	0.0259	1761 ± 77	1782 ± 215	1217 ± 80	1556 ± 148

Web Table 5 (58)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
203413_at	NET-6	transmembrane 4 superfamily member tetraspan NET-6	-0.0190	0.0033	-0.2954	0.2035	0.1661	4911 ± 740	4055 ± 797	2973 ± 346	3149 ± 780
217979_at	NETO2	neuropilin and tolloid-like 2	-0.0016	0.0002	-0.3553	0.0663	0.0369	3470 ± 405	2691 ± 451	2277 ± 298	1814 ± 427
218888_s_at	NEUROD1	neurogenic differentiation 1	-0.0017	0.0020	-0.1374	0.1561	0.0046	617 ± 68	501 ± 87	367 ± 35	279 ± 64
206282_at	NEUROD6	neurogenic differentiation 6	-0.0024	0.0087	-0.3558	0.0902	0.0017	681 ± 46	546 ± 94	334 ± 47	357 ± 71
220045_at	NFYC	nuclear transcription factor Y, Y	-0.0058	0.0007	-0.1649	0.4237	0.0141	1251 ± 143	1088 ± 203	552 ± 40	781 ± 176
202216_x_at	NGFRAP1	nerve growth factor receptor associated protein 1	-0.0018	0.0080	-0.2709	0.3458	0.0039	327 ± 28	343 ± 13	304 ± 17	215 ± 19
217993_s_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1	-0.0051	0.0000	-0.0980	0.0174	0.0616	4275 ± 1218	2004 ± 1573	1560 ± 1114	8777 ± 1681
218133_s_at	NIF3L1	NIF3 NCG1 interacting factor 3-like 1	-0.0289	0.1257	-0.4701	-0.2797	0.3518	413 ± 40	418 ± 61	301 ± 47	303 ± 95
202475_at	NIFIE14	seven transmembrane domain protein	-0.0038	0.1706	-0.0081	0.1416	0.1809	1663 ± 77	1554 ± 159	1268 ± 99	1392 ± 193
209075_s_at	NIFU	nitrogen fixation cluster-like	-0.0278	0.0597	-0.4466	0.1517	0.0328	4324 ± 578	3463 ± 363	2433 ± 141	3145 ± 109
217109_s_at	NIPSNAP1	nipsnap homolog 1	-0.2214	0.0386	0.2985	-0.4741	0.2267	1968 ± 141	1988 ± 146	1730 ± 237	1517 ± 148
218557_at	NIT2	Nit protein 2	-0.1438	0.0447	0.1931	0.3439	0.2335	346 ± 38	410 ± 36	326 ± 32	283 ± 46
201077_s_at	NJMU-R1	protein kinase Njmu-R1	-0.0095	0.0417	-0.1985	-0.3776	0.0001	1996 ± 74	1860 ± 49	1599 ± 43	1487 ± 108
203830_at	NME1	non-melanistic cells 1, protein expressed in	-0.0108	0.0074	-0.3828	-0.1864	0.0931	58 ± 6	59 ± 10	34 ± 10	37 ± 9
201577_at	NME2	non-melanistic cells 2, protein expressed in	-0.0002	0.0132	-0.0693	0.0805	0.0177	1677 ± 98	2013 ± 333	1526 ± 93	996 ± 222
201268_at	NMP200	nuclear matrix protein NMP200	-0.0145	0.0032	-0.2512	0.3514	0.0064	1952 ± 82	1698 ± 146	1798 ± 89	1366 ± 27
204239_s_at	NNAT	neuronatin	-0.0396	0.1151	0.0817	-0.3799	0.1211	1299 ± 171	1763 ± 335	1005 ± 133	1085 ± 222
203103_s_at	NNT	nicotinamide nucleotide transhydrogenase	-0.0341	0.0024	0.0429	0.3751	0.0176	1385 ± 113	1182 ± 120	1138 ± 89	879 ± 87
202784_s_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	-0.0013	0.0122	-0.1247	0.4157	0.0449	198 ± 31	156 ± 19	134 ± 16	103 ± 11
214321_at	NOV	nephroblastoma overexpressed gene	-0.1281	0.0404	0.2049	0.1919	0.2718	1006 ± 317	910 ± 184	678 ± 104	443 ± 104
211951_at	NP25	neuronal protein	-0.0409	0.0022	-0.3290	0.3990	0.0121	1501 ± 60	1406 ± 72	1202 ± 68	1241 ± 78
39548_at	NPAS2	neuronal PAS domain protein 2	-0.0133	0.0117	0.0311	0.4752	0.0715	177 ± 11	187 ± 20	172 ± 9	137 ± 4
209460_at	NPD009	NPD009 protein	-0.1446	0.0279	-0.1857	0.1349	0.0610	2303 ± 212	1766 ± 64	2044 ± 227	1564 ± 55
39549_at	NPY	neuropeptide Y	-0.0119	0.0014	-0.2237	0.2086	0.0114	522 ± 41	458 ± 64	499 ± 29	309 ± 42
210519_s_at	NQO1	NADH dehydrogenase, quinone 1	-0.0358	0.2118	-0.1587	0.2682	0.3495	642 ± 66	552 ± 39	532 ± 43	522 ± 42
204791_at	NR2C1	nuclear receptor subfamily 2, group C, member 1	-0.0041	0.1308	-0.4607	-0.3655	0.2050	472 ± 19	454 ± 23	431 ± 13	402 ± 36
204031_at	NRGN	neurogranin	-0.1228	0.0144	0.4557	0.4226	0.1521	7959 ± 1379	7205 ± 1175	1415 ± 1423	3975 ± 469
206001_at	NRIP1	nuclear receptor interacting protein 1	-0.0072	0.0138	-0.3774	0.2133	0.0026	1142 ± 89	1099 ± 195	535 ± 42	672 ± 126
205999_s_at	NRN1	neurtin 1	-0.0066	0.0128	-0.4870	0.1262	0.0152	1262 ± 102	1025 ± 115	1138 ± 41	818 ± 96
209914_s_at	NRXN1	neurexin 1	-0.0029	0.0383	-0.0535	0.1016	0.0756	560 ± 66	470 ± 78	368 ± 45	327 ± 72
216096_s_at	NSAP1	NS1-associated protein 1	-0.0097	0.0029	0.1970	-0.2620	0.0116	283 ± 34	184 ± 19	191 ± 8	176 ± 21
209025_s_at	NT5E	5'-nucleotidase, ecto	-0.0216	0.0264	0.0432	-0.0668	0.0043	421 ± 21	441 ± 42	415 ± 40	255 ± 20
208093_s_at	NUDEL	LIS1-interacting protein NUDEL, endooligopeptidase A	-0.1093	0.0245	-0.0876	0.4134	0.1349	1368 ± 79	1202 ± 169	1170 ± 142	954 ± 78
203939_at	NUDT11	nucleic acid type motif 11	-0.0245	0.0286	-0.2781	0.1989	0.0176	201 ± 9	220 ± 22	193 ± 30	116 ± 22
219855_at	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	-0.0020	0.0004	-0.1390	0.4005	0.1961	822 ± 117	698 ± 107	530 ± 129	530 ± 81
205136_s_at	NUP153	nucleoporin 153kDa	-0.0020	0.0369	-0.2454	-0.1031	0.0055	524 ± 17	536 ± 22	481 ± 19	437 ± 10
202097_at	OAT	ornithine aminotransferase	-0.0134	0.0004	-0.2728	0.2734	0.0651	831 ± 37	871 ± 83	777 ± 38	662 ± 53
201364_s_at	OAZ2	ornithine decarboxylase antizyme 2	-0.1004	0.0379	-0.0793	0.3236	0.2038	1194 ± 102	1069 ± 117	1035 ± 83	847 ± 150
212461_at	OAZIN	ornithine decarboxylase antizyme inhibitor	-0.0493	0.0727	0.3947	0.3702	0.1639	1273 ± 105	1195 ± 142	978 ± 74	997 ± 87

Web Table 5 (59)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
201599_at	ODZ1	odt, odd Oz/ten-m homolog 1	-0.0105	0.0067	0.4922	0.0457	0.0057	3989 ± 367	3826 ± 163	3166 ± 292	2391 ± 306
205728_at	OGT	O-linked N-acetylglucosamine transferase	-0.0164	0.0062	-0.0712	0.3985	0.0306	386 ± 51	257 ± 15	252 ± 40	215 ± 33
205591_at	OLFM1	olfactomedin 1	-0.0251	0.0739	-0.4644	0.0994	0.3652	6279 ± 762	5627 ± 798	5286 ± 494	4436 ± 725
207093_s_at	OMG	oligodendrocyte myelin glycoprotein	-0.0165	0.2818	-0.3327	-0.2008	0.5925	2977 ± 180	3050 ± 321	2794 ± 229	2606 ± 241
214306_at	OPA1	optic atrophy 1	-0.2031	0.0313	-0.3732	0.0246	0.1938	883 ± 65	859 ± 76	909 ± 91	677 ± 49
212213_x_at	ORC3L	origin recognition complex, subunit 3-like	-0.0418	0.0265	-0.3638	0.0986	0.0276	1940 ± 198	1709 ± 69	1346 ± 122	1362 ± 141
204957_at	ORC5L	origin recognition complex, subunit 5-like	-0.0425	0.0823	-0.0323	0.3690	0.4154	562 ± 18	506 ± 62	497 ± 34	462 ± 48
219073_s_at	OSBPL10	oxysterol binding protein-like 10	-0.0608	0.0010	-0.3575	0.4733	0.0007	324 ± 34	288 ± 50	325 ± 28	124 ± 14
210028_s_at	OXCT	3-oxoacid CoA transferase	-0.0078	0.0054	-0.4835	0.0662	0.0397	441 ± 40	384 ± 36	428 ± 38	288 ± 58
202780_at	OXR1	oxidation resistance 1	-0.0106	0.0157	0.3498	0.4755	0.0185	1429 ± 195	1041 ± 43	883 ± 85	849 ± 27
201832_s_at	P115	vesicle docking protein p115	-0.0128	0.0672	0.3007	0.4243	0.1143	978 ± 96	858 ± 150	654 ± 41	653 ± 13
218197_s_at	P125	Sec23-interacting protein p125	-0.0311	0.0019	0.0539	-0.4047	0.0559	406 ± 72	326 ± 53	244 ± 37	202 ± 38
209175_at	P17.3	neuronal protein 17.3	-0.0101	0.0456	-0.3456	0.2038	0.0041	343 ± 16	369 ± 23	308 ± 13	275 ± 10
200627_at	P23	inactive progesterone receptor, 23 kD	-0.0366	0.3229	-0.0748	-0.3196	0.5814	3814 ± 362	3739 ± 501	3559 ± 288	3082 ± 73
218320_s_at	P311	P311 protein	-0.0130	0.0255	0.4359	0.1730	0.2742	1269 ± 108	1360 ± 88	1223 ± 60	1086 ± 87
201310_s_at	P450RAI-2	cytochrome P450 reductase metabolizing protein	-0.0241	0.0082	-0.2780	-0.2836	0.0451	2591 ± 247	2064 ± 73	2288 ± 222	1723 ± 90
217831_s_at	p47	p47	-0.2827	0.0279	-0.0362	0.2512	0.2037	381 ± 39	345 ± 46	331 ± 24	270 ± 32
207543_s_at	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase, α1	-0.0110	0.0648	-0.0619	-0.3645	0.1284	784 ± 116	721 ± 66	660 ± 45	478 ± 72
207668_x_at	P5	protein disulfide isomerase-related protein	-0.0267	0.1825	-0.0037	0.2605	0.1631	884 ± 84	743 ± 92	855 ± 87	622 ± 45
219825_at	PAFAH1B1	platelet-activating factor acetylhydrolase, 1b, α subunit	-0.0166	0.0352	-0.0474	0.1346	0.0113	381 ± 68	348 ± 78	356 ± 59	89 ± 32
200813_s_at	PAIP1	polyadenylate binding protein-interacting protein 1	-0.0129	0.0117	-0.4800	0.4024	0.0989	1369 ± 154	1104 ± 121	1125 ± 90	890 ± 137
210076_x_at	PAI-RBP1	PAI-1 mRNA-binding protein	-0.0715	0.0091	-0.0828	0.0437	0.0003	760 ± 53	507 ± 44	562 ± 22	509 ± 26
209064_x_at	PAK3	p21-activated kinase 3	-0.0474	0.0005	-0.4297	0.0191	0.1220	2361 ± 246	1952 ± 195	2073 ± 83	1464 ± 407
219461_at	PAK6	p21-activated kinase 6	-0.1484	0.0085	0.1117	0.1009	0.1197	538 ± 46	472 ± 46	483 ± 60	363 ± 41
214607_at	PAM	peptidylglycine α-amidating monooxygenase	-0.0213	0.0125	-0.4008	0.3293	0.0403	3105 ± 117	2810 ± 340	2598 ± 311	2016 ± 192
218771_at	PANK4	pantothenate kinase 4	-0.4583	0.0294	-0.3618	-0.3598	0.1265	363 ± 31	373 ± 34	327 ± 25	274 ± 19
204715_at	PANX1	pannexin 1	-0.0343	0.0906	-0.0089	0.2841	0.0762	164 ± 17	120 ± 22	111 ± 6	102 ± 22
212959_x_at	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	-0.0002	0.0016	-0.2800	0.2760	0.0704	2255 ± 227	1815 ± 329	1599 ± 204	1329 ± 226
209043_at	PC326	PC326 protein	-0.0039	0.0071	0.4994	0.3565	0.0100	2555 ± 140	2424 ± 222	2112 ± 97	1703 ± 237
221727_at	PC4	activated RNA polymerase II transcription cofactor 4	-0.0078	0.0122	-0.3851	0.1149	0.0283	2553 ± 473	2166 ± 448	1397 ± 195	967 ± 194
203860_at	PCCA	propionyl Coenzyme A carboxylase, α polypeptide	-0.0499	0.1059	-0.1605	0.1538	0.1963	297 ± 18	247 ± 22	226 ± 21	243 ± 39
212857_x_at	PCCB	propionyl Coenzyme A carboxylase, β polypeptide	-0.0015	0.0283	0.3702	-0.3935	0.0489	4244 ± 257	3621 ± 495	3166 ± 296	2818 ± 434
212694_s_at	PCDH11X	protocadherin 11 X-linked	-0.0049	0.0251	-0.0580	-0.3601	0.0763	356 ± 28	358 ± 47	271 ± 23	256 ± 37
210273_at	PCDH7	BH-protocadherin	-0.1650	0.0388	0.1026	0.3394	0.2562	873 ± 62	941 ± 114	771 ± 105	699 ± 54
210574_s_at	PCDHA12	protocadherin α 12	-0.0492	0.0954	-0.4893	-0.4816	0.2197	828 ± 93	707 ± 97	692 ± 62	589 ± 47
213558_at	PCLO	picolin	-0.1420	0.0107	-0.3489	0.1684	0.1069	2361 ± 276	2045 ± 296	2102 ± 266	1348 ± 186
203502_at	PCMT1	protein-L-isoaspartate O-methyltransferase	-0.0375	0.1014	0.4182	0.3935	0.3436	3286 ± 405	2972 ± 433	2490 ± 231	2460 ± 425
201202_at	PCNA	proliferating cell nuclear antigen	-0.0342	0.3086	-0.2987	-0.0732	0.4688	565 ± 54	534 ± 75	517 ± 65	409 ± 95
203660_s_at	PCNT2	pericentrin 2	-0.0063	0.1465	-0.0208	-0.4415	0.2669	1071 ± 43	995 ± 130	880 ± 55	890 ± 75

Web Table 5 (60)

Probe set	Name	Description	NFT _o	MMSE _o	NFT _i	MMSE _i	ANOVA	Control	Incipient	Moderate	Severe
205549_at	PCP4	Purkinje cell protein 4	-0.0731	0.0132	-0.3427	0.0067	0.0098	2632 ± 442	1385 ± 316	2131 ± 138	1094 ± 196
205825_at	PCSK1	proprotein convertase subtilisin/kexin type 1	-0.0760	0.0201	0.3026	0.3018	0.1015	359 ± 117	225 ± 62	185 ± 45	70 ± 20
210292_s_at	PCSK2	proprotein convertase subtilisin/kexin type 2	-0.0497	0.0120	-0.3257	-0.2192	0.0146	311 ± 36	217 ± 51	164 ± 25	143 ± 26
207239_s_at	PCTK1	PCTAIRE protein kinase 1	-0.1262	0.0343	-0.1361	0.1521	0.2667	547 ± 58	510 ± 70	507 ± 38	394 ± 17
221918_at	PCTK2	PCTAIRE protein kinase 2	-0.0434	0.2272	-0.3523	0.3467	0.5912	2675 ± 247	2329 ± 236	2336 ± 155	2201 ± 264
204869_at	PDCD2	programmed cell death 2	-0.0332	0.0098	0.4376	0.0683	0.0737	1857 ± 373	1579 ± 349	1418 ± 240	714 ± 96
213581_at	PDCD5	programmed cell death 5	-0.0162	0.0467	-0.2544	-0.2499	0.2017	407 ± 33	385 ± 25	339 ± 16	321 ± 43
204134_at	PDE2A	phosphodiesterase 2A, cGMP-stimulated	-0.1847	0.0032	0.2138	0.2123	0.0489	2889 ± 141	3178 ± 355	2889 ± 331	2049 ± 212
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	-0.0326	0.3534	-0.1073	-0.4451	0.4626	1664 ± 158	1521 ± 211	1541 ± 204	1219 ± 233
214130_s_at	PDE4DIP	phosphodiesterase 4D interacting protein	-0.0469	0.6333	-0.1268	-0.0530	0.6667	73 ± 19	68 ± 19	65 ± 14	42 ± 17
219275_at	PDHA1	pyruvate dehydrogenase α 1	-0.0043	0.0001	-0.0098	0.2160	0.1481	221 ± 13	199 ± 20	208 ± 18	150 ± 21
200980_s_at	PDHB	pyruvate dehydrogenase β	0.0000	0.0012	0.4392	-0.3941	0.0016	1331 ± 26	1249 ± 64	1146 ± 59	102 ± 43
203087_at	PDX1	Pyruvate dehydrogenase, lipoyl-containing X; E3-binding	-0.1471	0.0135	-0.4208	0.0339	0.1166	893 ± 86	775 ± 67	773 ± 53	630 ± 78
211023_at	PEG10	paternally expressed 10	-0.0050	0.0044	0.4320	-0.2444	0.0021	3184 ± 249	3117 ± 327	2159 ± 208	1813 ± 242
209242_at	PEG3	paternally expressed 3	-0.0608	0.0314	-0.2267	-0.3472	0.1349	6585 ± 539	5817 ± 759	5968 ± 512	4532 ± 618
213791_at	PENK	proenkephalin	-0.0085	0.3223	-0.0637	0.1760	0.1527	288 ± 19	252 ± 28	183 ± 30	260 ± 55
212094_at	PEX1	peroxisome biogenesis factor 1	-0.0231	0.0035	-0.2648	0.2707	0.1003	2795 ± 318	3278 ± 614	1807 ± 154	1498 ± 305
215023_s_at	PEX11B	peroxisomal biogenesis factor 11B	-0.0210	0.0114	0.4575	-0.2887	0.0214	132 ± 17	142 ± 26	96 ± 24	43 ± 14
202658_at	PEX3	peroxisomal biogenesis factor 3	-0.0283	0.3050	0.2090	-0.4465	0.1660	1041 ± 88	1127 ± 110	740 ± 73	799 ± 78
206420_at	PEX7	peroxisomal biogenesis factor 7	-0.1288	0.0469	0.4326	0.4238	0.1706	795 ± 47	832 ± 63	792 ± 58	669 ± 24
21507_at	PFDN1	prefoldin 1	-0.0804	0.0083	-0.0340	0.3985	0.0337	1546 ± 105	1423 ± 134	1446 ± 118	1053 ± 107
218336_at	PFDN2	prefoldin 2	-0.0160	0.0037	-0.4727	-0.2367	0.0399	288 ± 24	314 ± 16	215 ± 20	245 ± 35
203972_s_at	PFDN4	prefoldin 4	-0.0030	0.0021	-0.2792	0.2061	0.0154	466 ± 53	452 ± 70	383 ± 42	221 ± 20
205361_s_at	PFKM	phosphofructokinase, muscle	-0.0063	0.0173	-0.4324	0.3557	0.0159	3250 ± 260	2841 ± 286	2238 ± 289	2084 ± 244
210976_s_at	PFN2	profilin 2	-0.0062	0.0008	0.4195	0.2011	0.0682	10014 ± 859	3675 ± 1185	7037 ± 748	6590 ± 1195
204992_s_at	PFTK1	PFTAIRE protein kinase 1	-0.0082	0.0079	0.4874	0.0678	0.0263	2379 ± 154	2415 ± 218	2107 ± 182	1635 ± 192
204604_at	PGAM1	phosphoglycerate mutase 1	-0.0209	0.0344	-0.3238	0.1918	0.0493	6674 ± 616	5443 ± 351	5129 ± 395	4757 ± 510
200886_s_at	PGK1	phosphoglycerate kinase 1	-0.0012	0.0599	-0.1703	0.4710	0.2213	1613 ± 64	1554 ± 102	1436 ± 151	1305 ± 103
201868_s_at	PGM1	phosphoglucomutase 1	-0.0344	0.2342	-0.3081	0.2832	0.6955	3884 ± 251	3788 ± 559	3419 ± 222	3362 ± 464
211121_s_at	PGRMC1	progesterone receptor membrane component 1	-0.0119	0.0730	-0.0015	0.0068	0.1517	380 ± 20	315 ± 21	302 ± 39	259 ± 55
219394_at	PGS1	phosphatidylglycerophosphate synthase	-0.0116	0.0043	-0.3625	0.1837	0.0812	3233 ± 352	2505 ± 356	2002 ± 222	2079 ± 536
200738_s_at	PH-4	putative proline 4-hydroxylase	-0.0012	0.0927	-0.0597	0.3532	0.4203	321 ± 13	300 ± 25	274 ± 23	272 ± 34
210191_s_at	PHTF1	putative homeodomain transcription factor 1	-0.0438	0.9802	0.3200	-0.2490	0.2407	645 ± 37	644 ± 39	535 ± 40	662 ± 75
217862_at	PIAS1	protein inhibitor of activated STAT, 1	-0.0156	0.0312	-0.1491	-0.4629	0.0173	2289 ± 154	2043 ± 127	1689 ± 70	1770 ± 168
222125_s_at	PIGB	phosphatidylinositol glycan, class B	-0.0265	0.4780	-0.2272	-0.4830	0.6416	483 ± 30	502 ± 70	422 ± 64	428 ± 40
209707_at	PIGK	phosphatidylinositol glycan, class K	-0.0091	0.0388	-0.4914	0.1408	0.0281	818 ± 64	713 ± 54	795 ± 85	527 ± 22
214152_at	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	-0.0226	0.0073	-0.4351	0.2147	0.2305	579 ± 38	577 ± 28	526 ± 41	475 ± 46
212740_at	PIK4CA	phosphatidylinositol 4-kinase, catalytic, α polypeptide	-0.0149	0.0411	-0.1314	-0.2358	0.0169	1741 ± 224	1294 ± 76	1108 ± 121	1053 ± 119
207081_s_at	PIN	dynein, cytoplasmic, light polypeptide 1									

Web Table 5 (61)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
209018_s_at	PINK1	PTEN induced putative kinase 1	-0.0835	0.0070	-0.4977	0.1649	0.1454	1321 ± 101	1254 ± 65	1192 ± 52	1067 ± 66
200703_at	PIP5K1B	phosphatidylinositol 4-phosphate 5-kinase, type I, β	-0.0047	0.0048	-0.3047	0.2102	0.1285	10172 ± 672	3066 ± 1571	1219 ± 1035	6224 ± 1413
205632_s_at	PIP5K1C	phosphatidylinositol 4-phosphate 5-kinase, type I, γ	-0.0484	0.0185	-0.4943	0.0280	0.0040	795 ± 62	784 ± 94	499 ± 25	560 ± 38
212518_at	PITPN	phosphatidylinositol transfer protein	-0.0361	0.0209	-0.3586	0.2206	0.1774	2340 ± 126	2152 ± 147	2124 ± 169	1847 ± 173
201191_at	PITPNB	phosphatidylinositol transfer protein, β	-0.0255	0.0044	0.4938	0.4076	0.1057	489 ± 53	419 ± 68	419 ± 38	280 ± 74
202522_at	PJA1	praja 1	-0.0081	0.0383	-0.3010	0.2193	0.0115	2399 ± 134	2343 ± 122	1950 ± 105	1958 ± 33
221171_s_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.0738	0.0180	-0.2567	0.4167	0.0097	246 ± 17	219 ± 32	253 ± 26	126 ± 19
218667_at	PLCB1	phospholipase C, β 1	-0.0004	0.0001	-0.1957	0.2023	0.0772	1719 ± 111	1664 ± 117	1259 ± 98	1443 ± 10
213222_at	PLCL2	phospholipase C-like 2	-0.0091	0.0147	-0.4156	0.2477	0.0011	5460 ± 376	4232 ± 431	3604 ± 419	2688 ± 564
213309_at	PLINP-1	papillomavirus L2 interacting nuclear protein 1	-0.0238	0.0199	-0.0635	0.1993	0.0640	412 ± 55	327 ± 76	232 ± 38	215 ± 49
212891_s_at	PLXNA1	plexin A1	-0.0472	0.0036	-0.2520	0.1091	0.0831	249 ± 28	192 ± 39	179 ± 26	138 ± 24
201682_at	PMPCB	peptidase β	-0.0375	0.0359	-0.0911	-0.3878	0.5202	1241 ± 63	1205 ± 125	1055 ± 84	1130 ± 110
214781_at	PNMA2	paraneoplastic antigen MA2	-0.0217	0.0420	-0.1991	0.3972	0.0084	396 ± 34	281 ± 28	306 ± 27	228 ± 34
212036_s_at	PNN	pinin, desmosome associated protein	-0.3193	0.0376	-0.3043	0.2412	0.1625	600 ± 32	564 ± 25	580 ± 39	485 ± 44
209598_at	POH1	26S proteasome-associated pof1 homolog	-0.0029	0.0101	0.3527	-0.2843	0.2358	5459 ± 569	4556 ± 780	4025 ± 669	3556 ± 747
212296_at	POLR2B	polymerase II polypeptide B, 140kDa	-0.0428	0.0314	-0.2466	-0.4642	0.0667	2288 ± 146	2228 ± 157	1924 ± 125	1752 ± 190
202306_at	POLR2G	polymerase II polypeptide G	-0.0254	0.0847	-0.2151	0.0849	0.0410	1643 ± 137	1460 ± 111	1187 ± 44	1378 ± 84
201803_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related gene	-0.0146	0.0129	-0.4616	-0.0801	0.1129	1187 ± 85	1058 ± 131	945 ± 48	887 ± 97
216242_x_at	POLR2K	polymerase II polypeptide K, 7.0kDa	-0.0281	0.0024	0.0954	-0.3703	0.0083	685 ± 82	869 ± 123	579 ± 24	439 ± 47
210830_s_at	PON2	paraoxonase 2	-0.0143	0.0971	-0.2201	-0.4042	0.2561	1418 ± 179	1234 ± 278	1158 ± 153	843 ± 179
217848_s_at	PP	pyrophosphatase	-0.0039	0.0898	-0.0177	0.2296	0.1549	4022 ± 416	3457 ± 163	2915 ± 234	3072 ± 483
202634_at	PPIA	peptidylprolyl isomerase A	-0.0026	0.0004	-0.1484	-0.4865	0.0185	850 ± 66	837 ± 57	789 ± 35	590 ± 69
201293_x_at	PPID	peptidylprolyl isomerase D	-0.0031	0.0032	-0.0556	0.1031	0.0596	13811 ± 850	2487 ± 1497	11851 ± 732	9640 ± 1095
204186_s_at	PPP1R11	protein phosphatase 1, regulatory subunit 11	-0.0162	0.0393	0.2221	0.0565	0.0046	331 ± 26	269 ± 33	218 ± 7	206 ± 23
201604_s_at	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	-0.0386	0.0340	0.3262	0.4527	0.0050	327 ± 24	276 ± 47	267 ± 28	137 ± 28
201603_at	PPP1R2	protein phosphatase 1, regulatory subunit 2	-0.0162	0.0003	0.2750	0.1201	0.1917	626 ± 80	592 ± 71	511 ± 33	437 ± 38
213465_s_at	PPP1R7	protein phosphatase 1, regulatory subunit 7	-0.1161	0.0246	0.2748	-0.4794	0.1228	782 ± 63	795 ± 100	677 ± 60	572 ± 50
202165_at	PPP2CA	protein phosphatase 2, catalytic subunit, α isoform	-0.0052	0.0001	-0.2934	0.0502	0.0165	444 ± 69	438 ± 54	333 ± 19	205 ± 24
208652_at	PPP2R2B	protein phosphatase 2, regulatory subunit B, β isoform	-0.0338	0.0017	0.3552	0.3446	0.0028	3155 ± 299	2770 ± 112	2256 ± 130	1841 ± 279
213849_s_at	PPP2R5C	protein phosphatase 2, regulatory subunit B, γ isoform	-0.0271	0.0457	-0.4563	0.3413	0.0079	2047 ± 202	1733 ± 163	1729 ± 118	1173 ± 44
201877_s_at	PPP2R5E	protein phosphatase 2, regulatory subunit B, ε isoform	-0.0039	0.0069	-0.2833	0.4574	0.2200	1900 ± 182	1677 ± 196	1504 ± 103	1420 ± 204
202457_s_at	PPP3CA	calcineurin A α	-0.0006	0.0001	-0.0580	0.0480	0.0048	8074 ± 589	6655 ± 800	5487 ± 477	4384 ± 825
202432_at	PPP3CB	protein phosphatase 3, catalytic subunit, β isoform	-0.0576	0.0170	-0.4889	0.4507	0.1383	4985 ± 606	4343 ± 765	3769 ± 498	2951 ± 582
204507_s_at	PPP3R1	calcineurin B, type I	-0.0086	0.0017	0.4935	0.0485	0.0136	405 ± 62	300 ± 50	227 ± 13	191 ± 39
204506_at	PPT1	palmitoyl-protein thioesterase 1	-0.0070	0.0049	-0.4510	-0.3620	0.0015	1234 ± 109	837 ± 95	799 ± 55	765 ± 55
200975_at	PRAX-1	peripheral benzodiazepine receptor-associated protein 1	-0.0440	0.0009	0.2981	0.0304	0.0099	3582 ± 178	3607 ± 118	3458 ± 197	2708 ± 232
39729_at	PRDX2	peroxiredoxin 2	-0.0596	0.0292	0.4614	0.2679	0.2009	3131 ± 291	2805 ± 242	2711 ± 227	2333 ± 241
201619_at	PRDX3	peroxiredoxin 3	-0.0177	0.0517	-0.2494	-0.4916	0.2653	1362 ± 178	1284 ± 186	1051 ± 125	927 ± 196
201923_at	PRDX4	peroxiredoxin 4	-0.0476	0.5869	-0.2450	-0.2642	0.5751	540 ± 48	557 ± 58	458 ± 49	503 ± 61

Web Table 5 (62)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
205839_s_at	preimplantation protein 3	-0.0031	0.0108	-0.2184	0.4381	0.0006	844 ± 41	664 ± 54	584 ± 28	595 ± 51
37950_at	prolyl endopeptidase	-0.0217	0.2065	0.3111	-0.2782	0.2606	137 ± 11	143 ± 11	130 ± 9	-111 ± 14
202918_s_at	protein kinase, cAMP-dependent, regulatory, type I, α	-0.0317	0.0096	-0.4853	0.3906	0.0288	544 ± 45	456 ± 51	424 ± 15	-356 ± 37
200605_s_at	protein kinase, cAMP-dependent, regulatory, type I, β	-0.0412	0.0086	-0.3807	0.3783	0.0619	2457 ± 401	2172 ± 408	1710 ± 255	1113 ± 134
212559_at	protein kinase, cAMP-dependent, regulatory, type II, β	-0.0013	0.0006	-0.3936	0.2274	0.0372	1397 ± 165	1280 ± 222	910 ± 122	778 ± 113
203680_at	protein kinase C, β1	-0.0086	0.0013	0.3263	0.2240	0.0030	1838 ± 216	1414 ± 188	1137 ± 59	873 ± 145
209678_s_at	protein kinase C, iota	-0.0329	0.0238	0.1049	-0.0685	0.0382	5398 ± 393	4710 ± 227	4601 ± 476	3284 ± 583
203376_at	pre-mRNA splicing factor 17	-0.0092	0.0119	-0.4112	0.0685	0.0150	1222 ± 122	1455 ± 156	1036 ± 72	900 ± 26
209440_at	phosphoribosyl pyrophosphate synthetase 1	-0.0032	0.0198	0.3166	-0.2424	0.0114	1291 ± 84	1174 ± 92	914 ± 73	1034 ± 68
209440_at	protease, serine, 25	-0.0184	0.0146	-0.4113	0.0533	0.0369	1058 ± 64	1066 ± 113	833 ± 62	826 ± 50
220892_s_at	phosphoserine aminotransferase	-0.0491	0.0753	-0.1058	-0.3851	0.2611	841 ± 138	796 ± 164	673 ± 145	444 ± 81
201676_x_at	proteasome subunit, α type, 1	-0.0012	0.0311	0.4155	0.4945	0.0166	1522 ± 193	1403 ± 166	1027 ± 83	856 ± 93
210759_s_at	proteasome subunit, α type, 5	-0.0135	0.0318	-0.1441	0.1051	0.0453	1422 ± 104	1402 ± 135	983 ± 83	1037 ± 209
216088_s_at	proteasome subunit, β type, 2	-0.0364	0.3534	-0.4082	-0.4917	0.3533	328 ± 26	269 ± 31	268 ± 26	263 ± 39
201274_at	proteasome subunit, β type, 3	-0.0010	0.0070	-0.0947	0.4506	0.0734	654 ± 50	536 ± 69	470 ± 29	484 ± 69
200039_s_at	proteasome subunit, β type, 4	-0.0061	0.0082	-0.3801	-0.3101	0.0264	1705 ± 102	1643 ± 163	1393 ± 92	1210 ± 27
202244_at	proteasome subunit, β type, 5	-0.0235	0.0762	-0.1313	0.1674	0.2781	2345 ± 170	2055 ± 204	1982 ± 150	1896 ± 171
208799_at	proteasome subunit, β type, 6	-0.0208	0.0767	-0.2765	0.1780	0.2478	1790 ± 120	1741 ± 233	1375 ± 72	1451 ± 255
208827_at	proteasome subunit, β type, 7	-0.0144	0.1035	-0.3002	-0.4680	0.2908	884 ± 55	876 ± 54	847 ± 50	742 ± 61
201068_s_at	proteasome 26S subunit, ATPase, 2	-0.0129	0.1136	-0.0444	0.1440	0.2789	1438 ± 71	1274 ± 133	1140 ± 94	1142 ± 183
201400_at	proteasome 26S subunit, ATPase, 6	-0.0338	0.0077	-0.4886	0.3569	0.0157	1653 ± 67	1735 ± 213	1418 ± 50	1133 ± 107
201699_at	proteasome 26S subunit, non-ATPase, 1	-0.0152	0.0113	-0.3002	-0.4475	0.0620	568 ± 51	521 ± 76	432 ± 43	347 ± 45
201198_s_at	proteasome 26S subunit, non-ATPase, 10	-0.0011	0.0029	-0.3606	0.3787	0.1306	1027 ± 50	1004 ± 89	929 ± 45	790 ± 102
208776_at	proteasome 26S subunit, non-ATPase, 11	-0.0151	0.2360	0.4594	-0.4007	0.1905	609 ± 92	492 ± 92	359 ± 55	447 ± 89
219485_s_at	proteasome 26S subunit, non-ATPase, 12	-0.0011	0.0283	-0.3907	0.4622	0.0140	1407 ± 136	1358 ± 121	1079 ± 55	894 ± 88
202353_s_at	proteasome activator subunit 3	-0.0073	0.0113	-0.3918	-0.1008	0.1301	1128 ± 91	1048 ± 100	890 ± 58	850 ± 119
218371_s_at	paraspeckle protein 1	-0.0227	0.2295	-0.1960	-0.3731	0.3266	549 ± 28	514 ± 43	473 ± 34	483 ± 24
218477_at	PTD011 protein	-0.0284	0.0700	-0.2274	-0.4150	0.1845	1798 ± 249	1474 ± 278	1369 ± 195	1097 ± 124
201433_s_at	phosphatidylserine synthase 1	-0.0302	0.1749	-0.3827	-0.4934	0.4870	1860 ± 40	1859 ± 149	1665 ± 77	1721 ± 151
209852_x_at	phosphatase and tensin homolog	-0.0081	0.0354	-0.0945	0.1344	0.0214	1029 ± 35	1063 ± 71	982 ± 28	851 ± 45
204897_at	prostaglandin H synthase 4	-0.0468	0.4669	-0.2958	-0.4613	0.3667	127 ± 10	104 ± 19	83 ± 16	97 ± 26
211711_s_at	prostaglandin H synthase 2	-0.0122	0.0023	-0.4138	0.0631	0.0260	190 ± 8	162 ± 9	150 ± 11	143 ± 14
206772_at	parathyroid hormone receptor 2	-0.0455	-0.7974	-0.2897	0.2555	0.5778	223 ± 24	173 ± 30	195 ± 17	215 ± 37
218083_at	protein tyrosine kinase 2 β	-0.0253	0.0204	0.4371	0.4251	0.0388	340 ± 39	335 ± 25	258 ± 33	195 ± 50
203110_at	pleiotrophin	-0.0123	0.0018	0.4156	0.1991	0.2382	1756 ± 172	1795 ± 196	1617 ± 131	1321 ± 180
221840_at	protein tyrosine phosphatase, receptor type, E	-0.0421	0.0803	-0.4168	0.4167	0.1692	1402 ± 155	1219 ± 85	1045 ± 48	1086 ± 144
209466_x_at	protein tyrosine phosphatase, receptor type, N polypeptide 2	-0.0116	0.0092	0.2051	0.4984	0.0347	1911 ± 127	1879 ± 143	1467 ± 182	1329 ± 98
210675_s_at	protein tyrosine phosphatase, receptor type, R	-0.5414	0.0276	-0.0436	0.0865	0.0904	325 ± 22	242 ± 31	262 ± 36	205 ± 38
205948_at	protein tyrosine phosphatase, receptor type, T	-0.1792	0.0374	-0.2485	-0.1760	0.0830	472 ± 37	575 ± 149	370 ± 48	250 ± 76

Web Table 5 (63)

		WO 2005/076939										PCT/US2005/003668									
Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe										
209694_at	PTS	6-pyruvyltetrahydropterin synthase	-0.0377	0.3707	-0.2676	0.3147	0.3071	1000 ± 84	912 ± 105	767 ± 64	912 ± 105										
206157_at	PTX3	penitoxin-related gene, rapidly induced by IL-1 β	-0.4309	0.0154	0.0565	0.3271	0.1006	90 ± 12	90 ± 12	52 ± 10	61 ± 17										
216221_s_at	PUM2	puntillo homolog 2	-0.0019	0.1107	-0.1846	0.3783	0.3095	2907 ± 93	2774 ± 186	2738 ± 125	2508 ± 196										
201706_s_at	PXF	peroxisomal farnesylated protein	-0.0344	0.0633	-0.4288	-0.4344	0.2202	524 ± 44	530 ± 76	454 ± 42	356 ± 92										
203079_s_at	QP-C	low molecular mass ubiquitinone-binding protein	-0.0017	0.0159	0.3653	-0.4912	0.1272	2407 ± 350	2392 ± 270	1937 ± 215	1481 ± 318										
201568_at	QPC1	glutaminyl-peptide cyclotransferase	-0.0363	0.0020	0.3897	0.0943	0.0604	3863 ± 229	3684 ± 223	3173 ± 248	2838 ± 390										
205174_s_at	RA410	vesicle transport-related protein	-0.0249	0.0036	0.3491	0.4578	0.0085	217 ± 29	163 ± 22	117 ± 15	115 ± 19										
200834_s_at	RAB11A	RAB11A, member RAS oncogene family	-0.0118	0.0546	-0.3705	-0.1627	0.1194	2222 ± 119	2025 ± 236	1824 ± 135	1635 ± 221										
204974_at	RAB3A	RAB3A, member RAS oncogene family	-0.1214	0.0215	0.1592	0.2433	0.2369	2346 ± 403	2236 ± 215	1790 ± 263	1548 ± 217										
210406_s_at	RAB6A	RAB6A, member RAS oncogene family	-0.0090	0.0055	0.4432	0.2787	0.0051	2944 ± 286	2568 ± 395	2005 ± 160	1470 ± 141										
201047_x_at	RAB7	RAB7, member RAS oncogene family	-0.0090	0.0281	-0.4386	0.2434	0.0552	3497 ± 310	3334 ± 381	2684 ± 230	2350 ± 356										
203150_at	RAB9P40	Rab9 effector p40	-0.0090	0.0439	0.0169	0.4948	0.0472	512 ± 48	657 ± 95	483 ± 21	425 ± 21										
201223_s_at	RAD23B	RAD23 homolog B	-0.1689	0.0391	-0.1518	-0.4530	0.1062	972 ± 52	853 ± 117	736 ± 55	741 ± 73										
209849_s_at	RAD51C	RAD51 homolog C (S. cerevisiae)	-0.0139	0.0691	-0.1173	0.0339	0.0009	481 ± 35	400 ± 15	289 ± 22	318 ± 48										
206066_s_at	RAGA	Ras-related GTP-binding protein	-0.0111	0.0018	-0.1173	0.0339	0.0009	481 ± 35	400 ± 15	289 ± 22	318 ± 48										
202100_at	RALB	Ras-related GTP-binding protein	-0.0113	0.0382	-0.4333	0.3324	0.1583	186 ± 30	211 ± 8	144 ± 25	128 ± 28										
201628_s_at	RANBP16	v-ral simian leukemia viral oncogene homolog B	-0.2550	0.0070	0.1221	-0.4137	0.0408	1048 ± 73	1144 ± 91	875 ± 60	857 ± 78										
201713_s_at	RANBP2	RAN binding protein 16	-0.0065	0.0124	-0.0669	-0.3912	0.0814	2592 ± 327	2187 ± 360	1542 ± 196	1702 ± 352										
200992_at	RANBP7	RAN binding protein 2	-0.0496	0.0016	-0.0119	0.1367	0.0027	939 ± 70	807 ± 36	833 ± 61	550 ± 65										
202583_s_at	RANBP9	RAN binding protein 7	-0.0019	0.0007	-0.0068	0.1707	0.0034	1226 ± 50	1083 ± 44	1061 ± 54	922 ± 37										
201774_s_at	RAP1	RAN binding protein 9	-0.0213	0.0406	-0.1058	-0.4213	0.0888	590 ± 41	531 ± 42	504 ± 46	420 ± 48										
209444_at	RAP1GDS1	TRF2-interacting telomeric RAP1 protein	-0.1245	0.0243	-0.3511	0.1460	0.0926	4273 ± 411	3538 ± 262	3286 ± 315	3120 ± 311										
219752_at	RASAL1	RAP1, GTP-GDP dissociation stimulator 1	-0.0218	0.2779	-0.1054	-0.3284	0.4242	1873 ± 104	1726 ± 188	1576 ± 78	1608 ± 177										
202033_s_at	RB1CC1	RAS protein activator like 1	-0.0425	0.0580	0.1507	0.1512	0.4003	754 ± 72	780 ± 94	662 ± 91	591 ± 45										
201092_at	RBBP7	RB1-inducible coiled-coil 1	-0.0016	0.0021	-0.0057	0.4574	0.0026	1687 ± 137	1333 ± 149	1271 ± 136	903 ± 84										
202034_x_at	RBMX	retinoblastoma binding protein 7	-0.0166	0.0044	0.0712	-0.2828	0.0203	1637 ± 59	1700 ± 153	1564 ± 72	1503 ± 118										
213762_x_at	RBX1	RNA binding motif protein, X chromosome	-0.0310	0.0156	-0.1546	-0.1673	0.0007	732 ± 69	605 ± 23	530 ± 32	523 ± 54										
218117_at	RC3	ring-box 1	-0.0101	0.0143	0.4879	-0.4419	0.0169	994 ± 74	1198 ± 83	816 ± 47	772 ± 13										
201485_s_at	RCN2	rabconnectin-3	-0.0494	0.1507	-0.4626	0.2110	0.3914	1113 ± 48	1088 ± 139	1073 ± 58	744 ± 50										
212820_at	RCOR	reticulocalbin 2, EF-hand calcium binding domain	-0.0025	0.0239	0.3852	-0.4732	0.0887	847 ± 150	659 ± 144	550 ± 98	591 ± 139										
212612_at	REC14	REST corepressor	-0.0082	0.0050	0.3048	-0.2285	0.0800	1364 ± 169	1180 ± 148	1004 ± 130	809 ± 160										
205091_x_at	RECQL	recombination protein REC14	-0.0363	0.2159	-0.3520	0.2599	0.2323	342 ± 20	326 ± 37	271 ± 24	254 ± 28										
219370_at	REPRIMO	RecQ protein-like	-0.0363	0.2159	-0.3520	0.2599	0.2323	108 ± 9	96 ± 14	105 ± 14	71 ± 16										
203209_at	RFC5	candidate mediator of the p53-dependent G2 arrest	-0.5890	0.0171	-0.4041	0.3631	0.0584	610 ± 74	586 ± 100	612 ± 86	307 ± 85										
221532_s_at	RFPL1S	replication factor C 5, 36.5kDa	-0.1559	0.0312	0.0806	0.1896	0.0191	310 ± 22	283 ± 18	219 ± 11	243 ± 27										
214408_s_at	RFPL3S	ret finger protein-like 1 antisense	-0.0030	0.0048	-0.4217	0.2010	0.0052	806 ± 72	987 ± 50	741 ± 84	519 ± 72										
202963_at	RFX5	ret finger protein-like 3 antisense	-0.0118	0.4082	-0.0807	-0.1593	0.6198	157 ± 12	153 ± 18	131 ± 18	135 ± 21										
38290_at	RGS14	regulatory factor X, 5	-0.0280	0.0640	0.4011	0.0520	0.3412	320 ± 25	315 ± 31	291 ± 13	243 ± 53										
202388_at	RGS2	regulator of G-protein signalling 14	-0.0056	0.0484	-0.2988	0.0201	0.0819	496 ± 50	410 ± 73	295 ± 29	362 ± 69										
		regulator of G-protein signalling 2, 24kDa	-0.0462	0.3204	-0.2343	0.0834	0.0360	1581 ± 225	886 ± 39	944 ± 75	1141 ± 242										

Web Table 5 (64)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Control	Incipient	Moderate	Severe
210138_at	RGS20	regulator of G-protein signaling 20	-0.0259	0.0456	-0.4349	0.0178	0.1560	700 ± 58	579 ± 48	604 ± 54	525 ± 54
204339_s_at	RGS4	regulator of G-protein signalling 4	-0.2501	0.0047	0.4753	0.0108	0.0627	710 ± 97	548 ± 40	577 ± 65	419 ± 40
204337_at	RGS7	regulator of G-protein signaling 7	-0.0070	0.0002	-0.4824	0.0579	0.0481	3414 ± 635	2857 ± 869	2061 ± 340	1082 ± 207
206290_s_at	RIMS2	regulating synaptic membrane exocytosis 2	-0.0039	0.0005	-0.0362	0.0617	0.0063	3660 ± 319	2949 ± 350	2458 ± 400	1779 ± 331
206984_s_at	RIT2	Ras-like without CAAX 2	-0.1110	0.0333	-0.4794	0.3233	0.1997	346 ± 59	261 ± 45	279 ± 56	176 ± 43
206137_at	RNF11	ring finger protein 11	-0.0032	0.0022	0.3984	-0.3914	0.0014	733 ± 45	580 ± 26	547 ± 79	341 ± 67
208924_at	RNF14	ring finger protein 14	-0.0106	0.0378	-0.2098	0.2334	0.0087	3692 ± 286	3342 ± 291	3132 ± 201	2377 ± 201
218528_s_at	RNF38	ring finger protein 38	-0.1884	0.0467	-0.2510	-0.1167	0.0268	1236 ± 53	1323 ± 46	1007 ± 41	1061 ± 126
209111_at	RNF5	ring finger protein 5	-0.0580	0.0416	-0.4001	0.3892	0.0834	753 ± 51	790 ± 41	726 ± 32	531 ± 125
201824_at	RNF6	ring finger protein 6	-0.0227	0.0067	0.3640	0.3373	0.2201	650 ± 41	605 ± 66	595 ± 35	508 ± 29
203403_s_at	RNMT	RNA methyltransferase	-0.0250	0.0035	0.3032	0.2629	0.0500	1619 ± 155	1603 ± 67	1251 ± 110	1112 ± 119
204426_at	RNP24	coated vesicle membrane protein	-0.0658	0.0373	-0.2685	0.0970	0.1209	170 ± 24	144 ± 26	165 ± 23	92 ± 21
202683_s_at	ROBO1	roundabout, axon guidance receptor, homolog 1	-0.0229	0.0273	-0.0276	0.2454	0.0350	1008 ± 65	1073 ± 77	978 ± 45	807 ± 45
213194_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	-0.0190	0.0339	-0.4821	0.0486	0.0965	984 ± 82	859 ± 86	870 ± 61	676 ± 103
202762_at	RPE	ribulose-5-phosphate-3-epimerase	-0.0228	0.0031	-0.1453	0.0405	0.2037	1227 ± 85	1081 ± 67	1081 ± 74	966 ± 109
221770_at	RPIP8	Rap2 interacting protein 8	-0.0387	0.0374	-0.4633	0.0552	0.0123	179 ± 24	155 ± 18	87 ± 15	98 ± 27
206196_s_at	RPL14	ribosomal protein L14	-0.0217	0.0004	-0.2493	0.0482	0.2763	5570 ± 362	5352 ± 569	4939 ± 628	4245 ± 543
221476_s_at	RPL15	ribosomal protein L15	-0.0292	0.1512	0.4066	0.3810	0.4572	9984 ± 466	9872 ± 444	9211 ± 408	9104 ± 585
200074_s_at	RPL31	ribosomal protein L31	-0.0052	0.0196	0.3355	0.4248	0.0006	2098 ± 88	2117 ± 133	2057 ± 86	1450 ± 105
213687_s_at	RPL35A	ribosomal protein L35a	-0.0619	0.0386	-0.2630	0.3339	0.2020	3892 ± 155	3954 ± 208	3485 ± 320	3167 ± 251
202079_x_at	RPL38	ribosomal protein L38	-0.1238	0.0136	-0.0222	-0.4213	0.0234	12727 ± 476	12211 ± 521	12152 ± 629	10199 ± 636
213689_x_at	RPL5	ribosomal protein L5	-0.0137	0.1197	-0.0144	0.2009	0.1555	2350 ± 106	2050 ± 227	1983 ± 71	1911 ± 169
216044_x_at	RPL6	ribosomal protein L6	-0.0033	0.0230	-0.0440	-0.3552	0.0602	1544 ± 83	1545 ± 151	1264 ± 139	1145 ± 106
208689_s_at	RPN2	ribophorin II	-0.0299	0.3807	-0.0149	0.4547	0.5514	1178 ± 115	1022 ± 100	992 ± 91	995 ± 127
209482_at	RPP20	POP7 homolog	-0.0405	0.1971	-0.4286	0.3070	0.0432	621 ± 52	564 ± 48	436 ± 6	537 ± 47
203436_at	RPP30	ribonuclease P	-0.0199	0.1517	-0.0989	0.0653	0.4253	511 ± 33	503 ± 35	450 ± 38	448 ± 30
200834_s_at	RPS21	ribosomal protein S21	-0.0218	0.0785	-0.0662	0.4424	0.1528	7013 ± 172	6143 ± 780	5753 ± 580	5211 ± 561
217533_s_at	RPS26	ribosomal protein S26	-0.0237	0.5177	0.3376	-0.2461	0.2265	3324 ± 215	3747 ± 252	3794 ± 440	2763 ± 521
201875_at	RSN	reslin	-0.1203	0.0322	0.1531	-0.0849	0.0286	1621 ± 129	1694 ± 183	1670 ± 122	1092 ± 159
201980_s_at	RSU1	Ras suppressor protein 1	-0.0709	0.0021	-0.0167	0.2310	0.0132	451 ± 29	417 ± 11	343 ± 29	345 ± 25
200034_s_at	RTN1	reticulon 1	-0.0471	0.1056	-0.3376	0.2732	0.0280	5621 ± 278	4976 ± 478	5064 ± 363	3918 ± 311
204217_s_at	RTN2	reticulon 2	-0.0274	0.0350	-0.3646	-0.3413	0.0198	380 ± 28	354 ± 46	382 ± 39	277 ± 33
210222_s_at	RTN3	reticulon 3	-0.0035	0.0758	-0.1239	-0.3497	0.1659	4900 ± 755	4110 ± 829	2660 ± 465	2077 ± 507
211509_s_at	RTN4	reticulon 4	-0.0146	0.1005	-0.1391	0.0016	0.0074	12171 ± 355	12167 ± 350	11415 ± 534	10560 ± 855
212438_at	RY1	putative nucleic acid binding protein RY-1	-0.0161	0.0028	-0.3721	-0.3424	0.0075	600 ± 51	452 ± 21	410 ± 32	478 ± 25
212440_at	SACS	spastic ataxia of Charlevoix-Saguenay	-0.0582	0.0179	-0.4237	0.2564	0.0747	1292 ± 90	1307 ± 103	1090 ± 100	817 ± 83
208742_s_at	SAP18	sin3-associated polypeptide, 18kDa	-0.0037	0.3238	-0.0208	0.4136	0.3122	1663 ± 153	1465 ± 205	1176 ± 93	1051 ± 229
210592_s_at	SAT	spermidine/spermine N1-acetyltransferase	-0.0282	0.2729	-0.4559	0.3318	0.5457	5993 ± 501	5236 ± 280	4845 ± 324	4789 ± 827
211423_s_at	SC5DL	sterol-C5-desaturase-like	-0.0282	0.2729	-0.4559	0.3318	0.5457	1344 ± 119	1279 ± 120	1121 ± 118	1147 ± 156

Web Table 5 (65)

PCT/US2005/003668

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Control	Incipient	Moderate	Severe
203231_s_at	SCA1	-0.0856	0.0133	0.2071	0.3996	0.0007	558 ± 96	727 ± 98	183 ± 16	366 ± 95
213262_at	SCAMP1	-0.0127	0.0479	-0.1433	0.0913	0.0066	1103 ± 93	1018 ± 94	1022 ± 53	700 ± 54
206668_s_at	SCAP2	-0.0488	0.0290	0.2270	-0.2586	0.2039	126 ± 19	102 ± 16	78 ± 8	89 ± 23
204382_at	SCG3	-0.0078	0.0063	-0.2109	0.1617	0.1435	369 ± 31	365 ± 34	305 ± 23	284 ± 34
204030_s_at	SCHIP1	-0.0223	0.3671	0.4623	0.2794	0.2567	3214 ± 223	3205 ± 161	2592 ± 226	2927 ± 341
219196_at	SCN1A	-0.0476	0.0119	-0.2714	-0.3141	0.0411	477 ± 64	352 ± 62	301 ± 59	220 ± 61
210383_at	SCN2A2	-0.0438	0.0207	0.2869	-0.0713	0.0931	684 ± 46	640 ± 141	531 ± 42	392 ± 75
206381_at	SCN3A	-0.0154	0.0222	-0.0122	0.1496	0.0865	372 ± 43	390 ± 64	279 ± 27	236 ± 51
201339_s_at	SCP2	-0.0225	0.0592	-0.3626	-0.4427	0.1686	810 ± 64	780 ± 119	612 ± 64	570 ± 105
205475_at	SCRG1	-0.0080	0.0694	-0.3106	0.3400	0.2099	3178 ± 354	2698 ± 308	2399 ± 387	2241 ± 220
210432_s_at	SDFR1	-0.0104	0.0127	-0.4237	-0.3692	0.0948	1177 ± 57	951 ± 143	1090 ± 179	673 ± 18
201093_x_at	SDHA	-0.0350	0.0601	-0.0064	0.2115	0.0214	797 ± 39	635 ± 87	501 ± 13	57 ± 92
202228_s_at	SDHB	-0.0024	0.0112	0.4220	0.2245	0.1056	8341 ± 809	7819 ± 1144	6616 ± 680	5052 ± 1179
202675_at	SDHD	-0.0209	0.0456	-0.0635	0.2201	0.0899	342 ± 25	352 ± 28	295 ± 26	229 ± 59
207707_s_at	SEC13L1	-0.0209	0.3417	-0.1791	0.4572	0.4523	800 ± 38	771 ± 77	678 ± 23	754 ± 81
201583_s_at	SEC23B	-0.1008	0.0249	-0.0902	0.0112	0.0198	477 ± 37	371 ± 28	355 ± 20	372 ± 24
221217_s_at	SEC3	-0.0085	0.1891	0.3149	-0.2923	0.3355	1597 ± 61	1554 ± 128	1483 ± 112	1315 ± 140
202026_at	SERPINI1	-0.0016	0.0009	-0.2028	0.2856	0.0484	638 ± 65	520 ± 67	408 ± 34	443 ± 72
205352_at	SEZ6L	-0.0017	0.0287	0.1193	0.4948	0.0022	3672 ± 534	2816 ± 496	1752 ± 119	1388 ± 284
201586_s_at	SFPQ	-0.1449	0.0385	0.4017	-0.4022	0.1683	665 ± 38	664 ± 108	550 ± 68	417 ± 108
200754_x_at	SFRS2	-0.0090	0.3495	-0.1754	-0.2958	0.4427	1753 ± 72	1710 ± 151	1426 ± 117	1540 ± 267
211894_x_at	SFRS3	-0.0360	0.0347	0.0935	-0.0057	0.0127	522 ± 37	589 ± 60	375 ± 32	419 ± 57
208673_s_at	SFRS5	-0.0366	0.0188	-0.1667	0.3371	0.0067	572 ± 40	699 ± 94	582 ± 32	360 ± 44
210077_s_at	SGNE1	-0.0321	0.0105	-0.4921	0.1795	0.0230	173 ± 33	140 ± 17	154 ± 19	60 ± 13
201312_s_at	SH3BGR1	-0.0051	0.1004	-0.4690	-0.1642	0.1710	3263 ± 211	3215 ± 450	2635 ± 204	2465 ± 307
218813_s_at	SH3GLB2	-0.0508	0.0307	-0.4020	0.4245	0.0711	547 ± 41	600 ± 36	562 ± 30	426 ± 62
203889_at	SH3YL1	-0.0266	0.0374	-0.2030	-0.4626	0.0527	4541 ± 661	3594 ± 522	2643 ± 367	2566 ± 613
204019_s_at	SHANK2	-0.0010	0.0004	-0.2355	0.3404	0.0761	1622 ± 47	1566 ± 129	1560 ± 104	1283 ± 92
206330_s_at	SHC3	-0.3411	0.0492	-0.2830	-0.4775	0.1666	377 ± 82	386 ± 75	394 ± 107	138 ± 37
201381_x_at	SIP	-0.0042	0.0044	-0.1175	0.0358	0.0727	2353 ± 238	2264 ± 116	1901 ± 161	1598 ± 235
217761_at	SIPL	-0.0337	0.3120	0.1095	-0.0294	0.2446	1109 ± 72	1187 ± 113	994 ± 56	981 ± 53
211761_s_at	SIRT3	-0.0413	0.0253	-0.4400	-0.2261	0.1357	3044 ± 308	2671 ± 295	2194 ± 185	2334 ± 283
221562_s_at	SLC12A5	-0.0237	0.0048	-0.4712	0.4585	0.0463	312 ± 22	281 ± 42	296 ± 29	192 ± 29
210040_at	SLC1A1	-0.0050	0.0024	-0.4417	0.1041	0.0310	4065 ± 592	3201 ± 518	2646 ± 410	1941 ± 338
209610_s_at	SLC1A4	-0.0626	0.0145	0.1458	0.2202	0.0557	1176 ± 82	1415 ± 179	1147 ± 143	862 ± 101
213664_at	SLC21A14	-0.0361	0.0154	0.2701	-0.1302	0.0197	1294 ± 135	1000 ± 111	894 ± 86	749 ± 136
220460_at	SLC25A11	-0.0291	0.0275	-0.3200	0.3830	0.0478	1341 ± 118	1405 ± 217	1155 ± 173	796 ± 68
203340_s_at	SLC25A12	-0.0207	0.0246	-0.3285	0.2534	0.0006	663 ± 59	551 ± 57	434 ± 36	335 ± 40
203339_at	SLC25A14	-0.0199	0.0192	-0.3401	0.0667	0.0243	664 ± 104	492 ± 72	333 ± 27	410 ± 48

Web Table 5 (66)

Upregulated

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
204177_s_at	Kelch motif containing protein	0.0017	-0.0012	0.0959	-0.0389	0.0023	344 ± 23	396 ± 11	498 ± 32	504 ± 50
AB026190	ATP-binding cassette, sub-family A (ABC1), member 1	0.0009	-0.0024	0.0432	-0.2938	0.0084	802 ± 124	1093 ± 209	1153 ± 127	2307 ± 574
203505_at	adenylate cyclase 7	0.0464	-0.0129	0.1193	-0.0061	0.1919	228 ± 33	311 ± 39	292 ± 20	340 ± 56
203741_s_at	adducin 3 (gamma)	0.0071	-0.0032	0.0287	-0.0699	0.0009	4514 ± 321	5928 ± 566	8335 ± 749	7237 ± 742
ADD3	zinc finger protein	0.0143	-0.2315	0.0427	-0.0670	0.3397	496 ± 25	506 ± 21	596 ± 66	564 ± 46
AF020591	N-acetylglucosamine-phosphate mutase	0.8955	-0.0164	-0.1862	-0.0265	0.3263	259 ± 27	313 ± 56	322 ± 39	400 ± 80
AGM1	angiotensin II receptor, type 1	0.0017	-0.0003	0.1517	-0.0147	0.0076	79 ± 6	105 ± 14	122 ± 10	138 ± 15
AGTR1	angiotensin II receptor-like 1	0.0444	-0.0459	0.0168	-0.0327	0.0253	897 ± 172	1599 ± 422	3549 ± 921	2433 ± 627
AGTRL1	absent in melanoma 1	0.1970	-0.0054	0.0184	-0.1655	0.0408	177 ± 19	215 ± 22	218 ± 13	289 ± 47
AIM1	A kinase (PRKA) anchor protein 13	0.0059	-0.0026	0.0412	-0.0187	0.0097	441 ± 42	513 ± 52	641 ± 79	869 ± 138
AKAP13	A kinase (PRKA) anchor protein (yoliao) 9	0.1518	-0.0230	0.0615	-0.0231	0.0890	205 ± 45	275 ± 27	408 ± 75	354 ± 77
AKAP9	Alstrom syndrome 1	0.0641	-0.0127	0.0028	-0.0399	0.1605	160 ± 17	203 ± 18	228 ± 23	252 ± 57
ALMS1	angiopoietin 1	0.0907	-0.0043	0.1258	-0.0190	0.1030	346 ± 42	388 ± 76	523 ± 89	556 ± 67
ANGPT1	angiopoietin-like 2	0.0000	-0.0393	0.0122	-0.1088	0.0460	98 ± 8	133 ± 15	161 ± 8	173 ± 35
ANGPTL2	acidic (leucine-rich) nuclear phosphoprotein 32 B	0.0029	-0.0014	0.2229	-0.0488	0.0179	720 ± 86	850 ± 111	1215 ± 197	1253 ± 114
ANP32B	anti-oxidant protein 2	0.0819	-0.0387	0.0292	-0.4848	0.0547	2495 ± 180	2674 ± 239	4147 ± 588	3524 ± 606
AOP2	autophagy Apq3p/Aut1p-like	0.0750	-0.0209	0.0384	-0.1811	0.0440	60 ± 7	50 ± 9	91 ± 10	127 ± 38
APG3	apolipoprotein C-I	0.2519	-0.0489	0.0396	-0.3988	0.1150	1261 ± 161	1713 ± 237	1606 ± 135	1865 ± 143
APOC1	apolipoprotein C-IV	0.0014	-0.0267	0.0024	-0.2108	0.0482	179 ± 11	235 ± 25	281 ± 13	305 ± 60
APOC4	apolipoprotein L, 2	0.1087	-0.0013	0.0910	-0.0378	0.0066	162 ± 20	180 ± 13	256 ± 17	250 ± 30
APOL2	amyloid beta (A4) precursor protein	0.0085	-0.0024	0.0521	-0.0046	0.0319	345 ± 18	385 ± 28	458 ± 24	573 ± 108
APP	ADP-ribosylation factor 6	0.1885	-0.0027	0.3874	-0.0262	0.0753	143 ± 10	128 ± 26	181 ± 23	190 ± 11
ARF6	ADP-ribosylation factor GTPase activating protein 1	0.2345	-0.0486	0.1206	-0.0101	0.3263	602 ± 43	658 ± 36	744 ± 76	735 ± 84
ARFGAP1	Rho guanine nucleotide exchange factor (GEF) 15	0.5720	-0.0164	0.0480	-0.0151	0.0821	199 ± 18	235 ± 31	226 ± 24	295 ± 30
ARHGEF15	actin related protein 2/3 complex, subunit 18, 41kDa	0.0177	-0.0194	0.0218	-0.2238	0.1227	394 ± 26	492 ± 59	536 ± 56	553 ± 53
ARPC1B	type 1 TNF receptor shedding aminopeptidase regulator	0.1149	-0.0082	0.3852	-0.0417	0.1942	187 ± 26	199 ± 29	215 ± 10	267 ± 36
ARTS-1	achaele-scute complex-like 1 (Drosophila)	0.0416	-0.0042	0.0197	-0.1938	0.0184	353 ± 37	537 ± 111	502 ± 78	832 ± 153
ASCL1	activator of S phase kinase	0.8717	-0.0304	0.0294	-0.2094	0.3078	107 ± 7	97 ± 10	110 ± 7	126 ± 14
ASK	ATPase, Class V, type 10D	0.1324	-0.0307	0.0384	-0.2089	0.2592	289 ± 19	297 ± 28	317 ± 35	370 ± 39
ATP10D	ATPase, Class I, type 8B, member 1	0.0051	-0.0400	0.2453	-0.0306	0.0561	1259 ± 205	1462 ± 119	2399 ± 338	2176 ± 557
ATP8B1	BAI1-associated protein 3	0.1084	-0.0263	0.0289	-0.4828	0.1003	312 ± 19	353 ± 48	382 ± 25	433 ± 42
BAIAP3	B-cell CLL/lymphoma 7A	0.0260	-0.0016	0.0430	-0.0731	0.0023	744 ± 103	784 ± 87	1431 ± 127	1264 ± 199
BCL7A	biglycan	0.0134	-0.0022	0.0318	-0.0015	0.0133	424 ± 33	557 ± 32	544 ± 47	717 ± 94
BGN	BRCA1 associated protein	0.0364	-0.0024	0.0192	-0.0153	0.0087	177 ± 16	231 ± 19	241 ± 11	253 ± 17
BRAP	bromodomain containing 1	0.1618	-0.0103	0.2763	-0.0170	0.0053	556 ± 49	617 ± 46	776 ± 16	675 ± 36
BRD1	bombesin-like receptor 3	0.0584	-0.0210	0.0075	-0.0861	0.0734	119 ± 14	145 ± 15	163 ± 26	210 ± 32
BR3	chromosome 1 open reading frame 25	0.7491	-0.0408	0.3573	-0.0354	0.1346	177 ± 12	194 ± 27	175 ± 8	234 ± 24
C1orf25	chromosome 20 open reading frame 104	0.1491	-0.0113	0.0243	-0.0391	0.1277	882 ± 55	1015 ± 77	1019 ± 38	1102 ± 76
C20orf104										

Web Table 6 (1)

Probe set Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Cntrl	Incipient	Moderate	Severe
221827_at	chromosome 20 open reading frame 18	0.0144	-0.0221	0.0466	0.2796	0.0226	430 ± 28	456 ± 22	456 ± 64	622 ± 19
217622_at	chromosome 22 open reading frame 3	0.0401	-0.0221	0.0616	-0.0150	0.0752	120 ± 10	142 ± 29	204 ± 35	241 ± 52
205500_at	complement component 5	0.0406	-0.1233	0.2302	-0.0336	0.2194	183 ± 14	212 ± 19	240 ± 21	243 ± 38
48031_t_at	chromosome 5 open reading frame 4	0.0116	-0.0182	0.0422	-0.3703	0.0303	543 ± 35	755 ± 125	768 ± 54	975 ± 157
221766_s_at	chromosome 6 open reading frame 37	0.0579	-0.0121	0.1136	-0.0463	0.1911	184 ± 31	240 ± 41	285 ± 32	304 ± 57
204265_s_at	chromosome 8 open reading frame 9	0.0431	-0.0024	0.0892	-0.0046	0.0429	408 ± 44	471 ± 31	547 ± 41	622 ± 83
221543_s_at	chromosome 8 open reading frame 2	0.1488	-0.0194	0.0309	-0.1725	0.2136	763 ± 76	839 ± 29	884 ± 30	938 ± 58
214680_x_at	caldesmon 1	0.1284	-0.0197	0.0449	-0.0125	0.1927	103 ± 8	146 ± 15	162 ± 10	160 ± 43
213956_at	centrosome-associated protein 350	0.0676	-0.0213	0.0893	-0.0111	0.0257	326 ± 44	357 ± 29	624 ± 83	501 ± 116
211464_x_at	caspase 6, apoptosis-related cysteine protease	0.0005	-0.0328	0.2753	-0.0058	0.1579	104 ± 17	143 ± 17	189 ± 36	206 ± 58
212586_at	calpastatin	0.2290	-0.0017	0.0618	-0.0001	0.0238	947 ± 34	1222 ± 104	1143 ± 61	1316 ± 113
212014_x_at	CD44 antigen	0.1574	-0.0011	-0.3565	-0.0400	0.0246	202 ± 43	251 ± 20	345 ± 58	450 ± 76
205173_x_at	CD58 antigen	-0.6922	-0.0360	0.4973	-0.0105	0.6313	204 ± 23	219 ± 42	205 ± 38	270 ± 58
205288_at	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.0944	-0.0002	0.0000	-0.0166	0.0313	51 ± 5	68 ± 8	72 ± 8	99 ± 17
210473_s_at	cell division cycle 2-like 2	0.0022	-0.0040	0.0912	-0.0263	0.0661	718 ± 34	845 ± 83	1021 ± 146	1119 ± 136
214721_x_at	CDC42 effector protein (Rho GTPase binding) 4	0.0425	-0.0042	0.0381	-0.0265	0.1068	845 ± 77	1065 ± 139	1164 ± 62	1311 ± 225
209057_x_at	CDC5 cell division cycle 5-like (S. pombe)	0.3540	-0.0401	0.0015	-0.0797	0.1905	325 ± 20	385 ± 31	375 ± 41	437 ± 43
201938_at	CDK2-associated protein 1	0.4430	-0.0078	0.3673	-0.0038	0.2039	6126 ± 401	6628 ± 886	8130 ± 1006	8106 ± 951
204039_at	CCAAT/enhancer binding protein (C/EBP), alpha	0.0472	-0.1038	0.0184	0.4440	0.1807	597 ± 48	774 ± 100	786 ± 93	830 ± 61
214102_at	centaurin, delta 1	0.0056	-0.0098	0.0096	-0.1393	0.0116	395 ± 32	628 ± 62	696 ± 60	790 ± 141
219746_at	cer-d4 (mouse) homolog	0.0156	-0.0006	0.0173	0.4469	0.0000	294 ± 13	424 ± 62	382 ± 25	599 ± 35
211862_x_at	CASP8 and FADD-like apoptosis regulator	0.0629	-0.0129	0.0302	-0.0682	0.2689	270 ± 13	291 ± 33	329 ± 41	345 ± 18
203461_at	chromodomain helicase DNA binding protein 2	0.0015	-0.0001	0.1545	-0.0180	0.0000	143 ± 11	178 ± 33	184 ± 21	352 ± 35
221059_s_at	carbohydrate sulfotransferase 6	0.0221	-0.0014	0.0043	-0.4750	0.0086	650 ± 50	658 ± 70	926 ± 115	1061 ± 113
214135_at	claudin 18	0.0325	-0.1671	0.0338	0.4801	0.0680	123 ± 15	187 ± 22	172 ± 17	192 ± 27
204482_at	claudin 5	0.0230	-0.0576	0.0011	-0.3048	0.0121	684 ± 76	1053 ± 123	1262 ± 153	1111 ± 109
208559_at	chloride intracellular channel 1	0.8258	-0.0403	-0.2440	-0.0457	0.4004	486 ± 71	534 ± 50	627 ± 22	614 ± 94
222043_at	clusterin	0.0002	-0.0176	0.0040	0.0373	0.0226	1111 ± 60	982 ± 60	1716 ± 273	1584 ± 207
61732_t_at	capillary morphogenesis protein 1	0.1620	-0.0075	0.3686	-0.0276	0.0255	21 ± 4	31 ± 4	35 ± 5	62 ± 18
201774_s_at	chromosome condensation-related SMC-associ. prot. 1	0.0002	-0.0168	0.0069	-0.0166	0.2398	147 ± 18	152 ± 31	179 ± 13	203 ± 10
212189_s_at	component of oligomeric golgi complex 4	0.0119	-0.1525	0.0294	-0.4694	0.2053	335 ± 46	423 ± 42	448 ± 31	486 ± 82
52651_at	collagen, type VIII, alpha 2	0.0147	-0.0006	0.0083	-0.0204	0.0028	216 ± 20	311 ± 28	317 ± 24	355 ± 24
206100_at	carboxypeptidase M	0.1786	-0.0370	0.2926	-0.0122	0.1208	196 ± 25	301 ± 49	301 ± 53	346 ± 44
202118_s_at	copine III	0.0249	-0.0163	0.2366	-0.0141	0.0019	258 ± 28	317 ± 36	424 ± 17	345 ± 23
33132_at	cleavage and polyadenylation specific factor 1, 160kDa	0.0495	-0.1760	0.0362	-0.0518	0.0953	483 ± 39	707 ± 77	759 ± 73	713 ± 129
204264_at	camiline palmitoyltransferase II	0.1620	-0.0001	0.0063	-0.0319	0.0017	104 ± 6	133 ± 12	132 ± 13	177 ± 14
217552_x_at	complement component (3b/4b) receptor 1	0.1135	-0.0040	0.3839	-0.0237	0.0830	19 ± 7	35 ± 11	43 ± 13	63 ± 14
209716_at	colony stimulating factor 1 (macrophage)	0.2485	-0.0008	0.1086	-0.0167	0.0039	367 ± 39	506 ± 50	500 ± 44	722 ± 98
203575_at	casein kinase 2, alpha prime polypeptide	0.0004	-0.0530	0.0046	-0.1334	0.0685	370 ± 8	389 ± 13	459 ± 37	437 ± 31

Web Table 6 (2)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
204619_s_at	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	0.1038	-0.0247	0.0746	-0.0042	0.1689	389 ± 31	519 ± 63	575 ± 85	558 ± 53
219080_s_at	CTPS2	CTP synthase II	0.1321	-0.0001	0.0362	-0.2678	0.0003	93 ± 11	112 ± 11	109 ± 13	196 ± 24
206297_at	CTRC	chymotrypsin C (caldecrin)	0.3537	-0.0247	0.0352	-0.4192	0.0299	162 ± 22	195 ± 30	181 ± 29	293 ± 43
202087_s_at	CTSL	cathepsin L	0.5555	-0.0272	-0.4994	-0.4002	0.6177	647 ± 22	679 ± 62	733 ± 60	743 ± 80
202901_x_at	CTSS	cathepsin S	0.4358	-0.0489	0.0066	-0.0708	0.1185	95 ± 8	144 ± 18	134 ± 18	149 ± 22
201424_s_at	CUL4A	cullin 4A	0.0516	-0.0168	0.2723	-0.0061	0.0363	336 ± 21	386 ± 43	483 ± 46	441 ± 28
204309_at	CYP11A	cytochrome P450, subfamily XIA	0.1618	-0.0057	0.2667	-0.0285	0.0499	119 ± 12	143 ± 6	150 ± 6	175 ± 23
220432_s_at	CYP39A1	cytochrome P450, subfamily XXXIX 1	0.0859	-0.0161	0.0101	-0.1890	0.1692	31 ± 5	40 ± 9	45 ± 5	57 ± 12
208515_at	CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3	0.0923	-0.0010	0.0075	-0.3227	0.0230	124 ± 17	143 ± 30	229 ± 52	367 ± 94
207646_s_at	D1S155E	NRAS-related gene	0.0484	-0.1550	0.0010	-0.1643	0.3444	2687 ± 151	2897 ± 196	3029 ± 101	2993 ± 141
208878_at	DAO	D-amino-acid oxidase	0.2283	-0.0445	0.0137	-0.3370	0.0682	270 ± 15	335 ± 60	321 ± 32	432 ± 50
206324_s_at	DAPK2	death-associated protein kinase 2	0.0267	-0.0082	0.0943	-0.0030	0.0044	122 ± 15	174 ± 16	141 ± 7	267 ± 50
201623_s_at	DARS	aspartyl-tRNA synthetase	0.6838	-0.0082	0.0183	-0.0978	0.1298	1240 ± 48	1426 ± 57	1476 ± 115	1625 ± 181
209335_at	DCN	decorin	0.6224	-0.0495	0.4554	-0.0316	0.3997	246 ± 17	292 ± 13	282 ± 28	317 ± 47
208024_s_at	DGCR5	DiGeorge syndrome critical region gene 6	0.0406	-0.0081	0.0315	-0.1106	0.0821	771 ± 56	849 ± 30	1027 ± 59	835 ± 110
204383_at	DGSI	DiGeorge syndrome critical region gene DGS1	0.1312	-0.0282	0.4132	-0.0319	0.1687	276 ± 16	273 ± 19	319 ± 22	364 ± 41
206061_s_at	DICER1	Dicer1, Dcr-1 homolog (Drosophila)	0.0041	-0.1117	0.1679	-0.0180	0.4337	469 ± 33	533 ± 77	596 ± 59	637 ± 55
215529_x_at	DIP2	disco-interacting protein 2 (Brosophila) homolog	0.1211	-0.0191	0.0476	-0.0375	0.0790	600 ± 77	753 ± 83	844 ± 170	923 ± 226
208216_at	DLX4	distal-less homeobox 4	0.2943	-0.0442	0.0145	-0.0010	0.0125	118 ± 14	138 ± 11	154 ± 21	194 ± 30
208382_s_at	DMC1	DMC1 dosage suppressor of mck1 homolog	0.4498	-0.0042	0.1001	-0.0160	0.0358	121 ± 6	187 ± 24	132 ± 16	219 ± 34
222247_at	DXSS42	pulative X-linked retinopathy protein	0.0926	-0.0300	0.0236	-0.2869	0.0231	117 ± 8	141 ± 15	147 ± 13	175 ± 17
208713_at	E1B-AP5	E1B-55kDa-associated protein 5	0.0209	-0.1151	0.0798	-0.0423	0.4552	611 ± 39	810 ± 73	758 ± 39	837 ± 67
204464_s_at	EDNRA	endothelin receptor type A	0.1235	-0.0246	0.2269	-0.0413	0.2709	178 ± 16	211 ± 21	217 ± 22	229 ± 33
201843_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	0.0049	-0.0071	0.0496	-0.0812	0.0171	518 ± 50	673 ± 145	812 ± 189	935 ± 191
206580_s_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	0.0175	-0.1229	0.0238	-0.4644	0.1303	682 ± 79	701 ± 61	1081 ± 90	1051 ± 173
218287_s_at	EIF2C1	eukaryotic translation initiation factor 2C, 1	0.0499	-0.0125	0.2796	-0.0357	0.0402	476 ± 30	586 ± 56	592 ± 30	663 ± 89
217820_s_at	ENAH	enabled homolog (Drosophila)	0.0097	-0.0009	0.1249	-0.0004	0.0051	1003 ± 42	1081 ± 99	1448 ± 189	1348 ± 61
213579_s_at	EP300	E1A binding protein p300	0.4848	-0.0113	0.3343	-0.0202	0.3262	203 ± 25	266 ± 19	246 ± 21	348 ± 36
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	0.2567	-0.0210	0.0372	-0.0020	0.0745	813 ± 39	849 ± 102	1025 ± 88	1024 ± 174
212087_s_at	ERAL1	Era G-protein-like 1 (E. coli)	0.0126	-0.0033	-0.4232	-0.0457	0.0032	588 ± 26	656 ± 33	633 ± 55	783 ± 75
217941_s_at	ERBB2IP	erbB2 interacting protein	0.0076	-0.0039	0.0463	-0.1209	0.0003	2624 ± 324	3068 ± 269	4899 ± 635	4093 ± 386
203643_at	ERF	Ets2 repressor factor	0.0565	-0.0356	0.0192	-0.1737	0.1039	181 ± 32	363 ± 33	447 ± 52	420 ± 48
213873_at	ESDN	endothelial & sm. muscle derived neuropilin-like protein	0.0184	-0.0015	0.3634	-0.0204	0.0153	152 ± 10	205 ± 20	195 ± 16	256 ± 53
209214_s_at	EWSR1	Ewing sarcoma breakpoint region 1	0.0047	-0.0929	0.0357	-0.4982	0.0750	1151 ± 47	1317 ± 96	1371 ± 42	1466 ± 69
50376_at	EZF-2	endothelial zinc finger protein 2	0.2415	-0.0155	0.0442	-0.0761	0.0227	943 ± 78	1307 ± 234	1181 ± 136	1619 ± 228
203989_x_at	F2R	coagulation factor II (thrombin) receptor	0.0077	-0.0010	0.0692	-0.0475	0.0059	49 ± 8	67 ± 7	63 ± 10	100 ± 18
208962_s_at	FADS1	fatty acid desaturase 1	0.0042	-0.2095	0.0299	0.2812	0.1813	1176 ± 114	1536 ± 158	2085 ± 232	2454 ± 398
209405_s_at	FAM3A	family with sequence similarity 3, member A	0.0393	-0.0008	-0.3708	-0.0354	0.0410	267 ± 9	341 ± 45	397 ± 54	368 ± 52
202766_s_at	FBN1	fibrillin 1 (Marfan syndrome)						303 ± 25	313 ± 18	385 ± 24	395 ± 39

Web Table 6 (3)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
203184_at	FBN2	fibrillin 2 (congenital contractual arachnodactyly)	0.0038	-0.0005	0.0026	-0.1568	0.0004	.73 ± 8	100 ± 4	95 ± 10	156 ± 21
213940_s_at	FBP17	formin-binding protein 17	0.0310	-0.2360	0.0361	-0.1219	0.0597	266 ± 35	377 ± 65	485 ± 71	346 ± 52
214623_at	FBXW3	F-box and WD-40 domain protein 3	0.0084	-0.0163	0.0019	-0.0990	0.0179	34 ± 9	69 ± 18	80 ± 18	134 ± 35
204379_s_at	FGFR3	fibroblast growth factor receptor 3	0.0009	-0.0075	0.0018	-0.1005	0.0349	1925 ± 183	2388 ± 291	3023 ± 414	3684 ± 718
205305_at	FGL1	fibrinogen-like 1	0.0010	-0.0038	0.2055	-0.0102	0.0214	158 ± 14	189 ± 13	223 ± 23	286 ± 56
222065_s_at	FLII	flightless I homolog (Drosophila)	0.0534	-0.0288	-0.4035	-0.0297	0.2726	324 ± 17	359 ± 46	386 ± 10	395 ± 31
218993_at	FLJ10581	putative RNA methyltransferase	0.0125	-0.1307	0.1828	-0.0363	0.0507	348 ± 13	364 ± 13	329 ± 30	430 ± 36
218485_s_at	FLJ11320	GDP-ucose transporter 1	0.1421	-0.0224	0.1217	-0.0303	0.0163	182 ± 15	202 ± 12	180 ± 17	270 ± 33
218658_s_at	FLJ12934	likely ortholog of mouse actin-related protein 8 homolog	0.0081	-0.0206	0.0037	-0.1453	0.0018	205 ± 13	313 ± 38	300 ± 7	330 ± 21
207876_s_at	FLNC	filamin C, gamma (actin binding protein 280)	0.0000	-0.0031	0.0096	-0.2264	0.0220	286 ± 28	363 ± 88	487 ± 52	576 ± 96
218053_at	FNBP3	formin binding protein 3	0.0032	-0.0028	0.0247	-0.0094	0.0012	820 ± 51	979 ± 63	1334 ± 126	1194 ± 86
210608_s_at	FUT2	fucosyltransferase 2 (secretor status included)	0.0025	-0.0411	0.0107	-0.3321	0.0771	150 ± 8	165 ± 12	164 ± 13	209 ± 27
202419_at	FVT1	follicular lymphoma variant translocation 1	0.0037	-0.0255	0.2682	-0.0356	0.1621	1159 ± 84	1279 ± 108	1477 ± 108	1416 ± 139
212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.1121	-0.0214	0.2110	-0.0953	0.0766	729 ± 44	807 ± 99	1057 ± 118	954 ± 113
209414_at	FZR1	Fzr1 protein	0.0802	-0.0120	0.0051	-0.0004	0.0042	114 ± 9	162 ± 8	177 ± 15	194 ± 22
220886_at	GABRQ	gamma-aminobutyric acid (GABA) receptor, theta	0.1085	-0.0081	0.0039	-0.0035	0.0053	98 ± 11	188 ± 27	155 ± 13	205 ± 28
205354_at	GAMT	guanidinoacetate N-methyltransferase	0.0054	-0.0940	0.0021	-0.1239	0.1569	317 ± 31	370 ± 30	364 ± 43	478 ± 80
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.4795	-0.0005	0.4933	-0.0312	0.0459	84 ± 17	90 ± 16	154 ± 26	164 ± 33
206397_x_at	GDF1	growth differentiation factor 1	0.0007	-0.0021	0.0047	0.1810	0.0013	3388 ± 448	3988 ± 621	4835 ± 615	9008 ± 1706
201667_at	GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	0.0088	-0.0029	0.2614	-0.0394	0.0066	8527 ± 616	9294 ± 933	3145 ± 1106	1958 ± 1320
207034_s_at	GLI2	GLI-Kruppel family member GLI2	0.0394	-0.0013	0.0002	-0.0537	0.0125	53 ± 6	94 ± 16	93 ± 8	96 ± 9
204187_at	GMPR	guanosine monophosphate reductase	0.0020	-0.0003	-0.2771	-0.0474	0.0068	302 ± 34	346 ± 63	558 ± 102	663 ± 97
201180_s_at	GNAI3	G protein, alpha inhibiting activity polypeptide 3	0.1123	-0.0083	0.3466	-0.0228	0.0947	946 ± 113	1147 ± 112	1067 ± 82	1310 ± 81
204993_at	GNAZ	G protein, alpha polypeptide	0.0099	-0.0145	0.0088	-0.0983	0.0075	943 ± 54	1089 ± 18	1052 ± 71	1320 ± 104
201567_s_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	0.5147	-0.0185	0.4713	-0.0085	0.2212	740 ± 42	859 ± 75	879 ± 78	934 ± 62
213206_at	GOSR2	golgi SNAP receptor complex member 2	0.0171	-0.2925	0.3581	-0.0243	0.1655	82 ± 14	96 ± 16	139 ± 13	122 ± 31
211977_at	GPR107	G protein-coupled receptor 107	0.1652	-0.0414	0.0094	-0.4349	0.0648	280 ± 16	355 ± 44	305 ± 22	424 ± 61
206960_at	GPR23	G protein-coupled receptor 23	0.0237	-0.5581	0.0386	-0.0143	0.2369	61 ± 9	86 ± 17	97 ± 12	76 ± 12
208035_at	GRM6	glutamate receptor, metabotropic 6	0.1456	-0.0001	0.2317	-0.0015	0.0001	281 ± 17	306 ± 24	286 ± 29	492 ± 46
209945_s_at	GSK3B	glycogen synthase kinase 3 beta	0.0279	-0.0703	0.1326	-0.0481	0.0448	419 ± 24	548 ± 55	559 ± 18	616 ± 77
202451_at	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	0.0620	-0.0457	0.0252	-0.1414	0.0349	653 ± 49	743 ± 56	894 ± 63	815 ± 59
222104_x_at	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	0.0188	-0.0183	0.0120	-0.1941	0.0192	267 ± 26	447 ± 70	546 ± 75	523 ± 79
210891_s_at	GTF2I	general transcription factor II, i	0.2744	-0.0106	0.4968	-0.0119	0.0945	7358 ± 359	7783 ± 546	8911 ± 158	8478 ± 660
215093_at	H105E3	NAD(P) dependent steroid dehydrogenase-like; H105e3	0.0019	-0.0135	0.2719	-0.0205	0.0545	187 ± 12	219 ± 14	229 ± 11	258 ± 28
220936_s_at	H2AFJ	H2A histone family, member J	0.0934	-0.0112	0.4641	-0.0283	0.0453	95 ± 12	100 ± 17	91 ± 12	145 ± 16
212205_at	H2AV	histone H2A.F.Z variant	0.0383	-0.1289	0.1438	-0.0485	0.0417	3246 ± 90	3551 ± 178	4050 ± 157	3704 ± 314
211998_at	H3F3B	H3 histone, family 3B (H3.3B)	0.0179	-0.0191	0.0119	-0.3470	0.0432	1123 ± 66	1487 ± 171	1755 ± 138	1810 ± 328
220801_s_at	HAO2	hydroxyacid oxidase 2 (long chain)	0.1094	-0.0016	0.0467	-0.0357	0.0027	145 ± 12	200 ± 20	176 ± 20	288 ± 42
218662_s_at	HCAP-G	chromosome condensation protein G	0.2099	-0.0134	0.0298	-0.2702	0.0556	53 ± 6	80 ± 13	68 ± 17	107 ± 17

Web Table 6 (4)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
217965_s_at	HCNGP	transcriptional regulator protein	0.0073	-0.0217	0.0403	-0.4671	0.0494	306 ± 15	374 ± 52	394 ± 48	526 ± 88
212785_s_at	HDCMA18P	HDCMA18P protein	0.6277	-0.0403	0.3208	-0.0189	0.2753	437 ± 37	520 ± 45	520 ± 41	530 ± 30
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.1330	-0.0038	0.0403	-0.0463	0.0316	115 ± 19	177 ± 30	218 ± 39	245 ± 31
207585_s_at	HLALS	MHC, class II-like sequence	0.0540	-0.0034	0.1439	-0.0397	0.0099	56 ± 8	64 ± 11	59 ± 12	112 ± 18
203744_at	HMGB3	high-mobility group box 3	0.1438	-0.0269	0.0263	-0.0227	0.1632	568 ± 20	585 ± 30	642 ± 25	697 ± 79
205600_x_at	HOXB5	homeo box B5	0.0237	-0.0572	0.0509	-0.0233	0.0765	277 ± 24	379 ± 36	342 ± 31	461 ± 85
206194_at	HOXC4	homeo box C4	0.0040	-0.0004	0.0495	-0.0181	0.0030	153 ± 14	189 ± 20	167 ± 18	295 ± 46
203283_s_at	HSZST1	heparan sulfate 2-O-sulfotransferase 1	0.1550	-0.0449	0.0280	-0.0483	0.1457	182 ± 14	200 ± 27	245 ± 19	236 ± 25
217760_at	HSPC128	DIPB protein	0.3976	-0.0047	0.3018	-0.0278	0.0323	1139 ± 32	1173 ± 42	1158 ± 25	1397 ± 119
218826_at	HSNOV1	novel protein	0.0117	-0.0088	0.0375	-0.0022	0.0004	349 ± 28	544 ± 56	451 ± 31	590 ± 35
218936_s_at	HSPC128	HSPC128 protein	0.0594	-0.0119	0.3851	-0.0222	0.1222	325 ± 11	348 ± 31	354 ± 28	434 ± 50
213645_at	HSRTSBETA	rTS beta protein	0.0150	-0.2776	0.0081	0.3794	0.3304	368 ± 48	511 ± 95	669 ± 156	688 ± 233
208360_s_at	HSU88895	endog. retrovirus HD1, ORF1, ORF2, & putative envelope	0.4625	-0.0383	0.0816	-0.0392	0.2937	264 ± 28	302 ± 30	293 ± 30	372 ± 65
205556_x_at	HUMGT198A	GT198, complete ORF	0.0035	-0.0230	0.0304	-0.4651	0.0162	232 ± 15	335 ± 62	326 ± 26	402 ± 30
209292_at	ID4	inhibitor of DNA binding 4	0.4504	-0.0427	0.1727	-0.0110	0.2324	918 ± 142	1154 ± 160	1429 ± 245	1321 ± 192
205058_at	IDUA	iduronidase, alpha-L-	0.0112	-0.0736	0.1242	-0.0002	0.4207	136 ± 17	176 ± 24	178 ± 20	200 ± 48
214314_s_at	IF2	translation initiation factor IF2	0.0593	-0.0046	0.0239	-0.1421	0.0879	149 ± 21	176 ± 29	212 ± 36	264 ± 38
214569_at	IFNA5	interferon, alpha 5	0.2400	-0.0137	0.0216	-0.0291	0.0697	101 ± 10	117 ± 15	118 ± 13	175 ± 34
210354_at	IFNG	interferon, gamma	0.5036	-0.0139	0.0368	-0.0010	0.0536	110 ± 11	154 ± 22	119 ± 15	189 ± 32
204912_at	IL10RA	interleukin 10 receptor, alpha	0.0029	0.0000	0.0744	-0.0319	0.0006	247 ± 18	309 ± 23	333 ± 32	473 ± 57
209575_at	IL10RB	interleukin 10 receptor, beta	0.0476	-0.0406	0.0583	-0.0115	0.1471	180 ± 17	244 ± 21	233 ± 28	269 ± 43
201887_at	IL13RA1	interleukin 13 receptor, alpha 1	0.2556	-0.0087	0.1003	-0.0713	0.0294	618 ± 64	815 ± 64	768 ± 66	918 ± 79
205707_at	IL17R	interleukin 17 receptor	0.4245	-0.0297	0.0266	-0.2735	0.1405	427 ± 39	498 ± 53	540 ± 72	641 ± 77
206295_at	IL18	interleukin 18 (interferon-gamma-inducing factor)	0.2454	-0.0423	0.1406	-0.0014	0.3269	70 ± 13	88 ± 13	84 ± 10	109 ± 22
204116_at	IL2RG	interleukin 2 receptor, gamma	-0.8498	-0.0379	0.0390	-0.0105	0.4319	338 ± 34	394 ± 33	428 ± 30	421 ± 68
205945_at	IL6R	interleukin 6 receptor	0.3942	-0.0089	0.0431	-0.1237	0.0575	138 ± 14	157 ± 17	178 ± 15	204 ± 20
219843_at	IPP	intracisternal A particle-promoted polypeptide	0.0356	-0.0841	0.0191	-0.0551	0.1628	153 ± 22	226 ± 37	193 ± 14	241 ± 43
222126_at	IRS3L	insulin receptor substrate 3-like	0.0826	-0.0056	0.0235	-0.0016	0.0082	404 ± 19	573 ± 55	596 ± 59	611 ± 31
207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	0.0425	-0.2678	0.0411	-0.0151	0.3381	136 ± 15	197 ± 20	193 ± 37	212 ± 50
214660_at	ITGA1	integrin, alpha 1	0.0126	-0.0056	0.1753	-0.0072	0.0405	17 ± 2	23 ± 5	22 ± 5	49 ± 15
201656_at	ITGA6	integrin, alpha 6	0.3613	-0.0391	0.0840	-0.0130	0.3150	369 ± 34	501 ± 75	508 ± 78	516 ± 77
216331_at	ITGA7	integrin, alpha 7	0.0848	-0.0186	0.0047	0.4410	0.0169	794 ± 44	1013 ± 116	1377 ± 137	1358 ± 228
214020_x_at	ITGB5	integrin, beta 5	0.1007	-0.0029	0.4578	-0.0295	0.0715	301 ± 24	350 ± 54	414 ± 36	477 ± 75
207187_at	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	0.1097	-0.0084	0.1080	-0.0339	0.1091	400 ± 21	444 ± 30	438 ± 35	540 ± 66
37872_at	JRK	jerky homolog (mouse)	0.0757	-0.0002	0.0915	-0.0121	0.0076	283 ± 17	303 ± 17	339 ± 16	383 ± 26
203752_s_at	JUND	jun D proto-oncogene	0.0006	-0.0284	0.4697	-0.0494	0.1244	7987 ± 603	8307 ± 654	9983 ± 683	10792 ± 1603
220776_at	KCNJ14	K+ inwardly-rectifying channel, J 14	0.0166	-0.0011	0.0401	-0.0048	0.0048	110 ± 6	136 ± 12	132 ± 12	239 ± 47
220727_at	KCNK10	potassium channel, subfamily K, member 10	0.0043	-0.0101	0.0012	-0.1831	0.0120	126 ± 9	154 ± 21	153 ± 8	222 ± 33
219371_s_at	KLF2	Kruppel-like factor 2 (lung)	0.2745	-0.0500	0.0070	-0.3375	0.0592	463 ± 36	681 ± 121	637 ± 46	800 ± 116

Web Table 6 (5)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
214715_x_at	KR18	KRAB zinc finger protein KR18	0.0463	-0.0301	0.0298	-0.0290	0.1092	1839 ± 257	1919 ± 186	3117 ± 542	2720 ± 558
200914_x_at	KTN1	kinesin 1 (kinesin receptor)	0.0042	-0.0029	0.0276	-0.0678	0.0151	1603 ± 117	1988 ± 199	2350 ± 166	2475 ± 279
205116_at	LAMA2	laminin, α2	0.0478	-0.0026	0.0191	-0.0749	0.0316	114 ± 10	149 ± 20	142 ± 7	214 ± 42
202202_s_at	LAMA4	laminin, α4	0.0258	-0.1425	0.0166	-0.0851	0.2081	189 ± 23	243 ± 37	280 ± 26	251 ± 41
200771_at	LAMC1	laminin, γ1 (formerly LAMB2)	0.1222	-0.0068	-0.2206	-0.0491	0.2585	655 ± 58	659 ± 53	739 ± 48	831 ± 107
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.0871	-0.0053	0.3217	-0.0455	0.1730	249 ± 14	266 ± 32	308 ± 26	330 ± 40
202193_at	LIMK2	LIM domain kinase 2	0.0058	-0.0005	0.3244	-0.0156	0.0096	207 ± 22	238 ± 20	360 ± 64	402 ± 47
213779_at	LOC129080	putative enu1	0.0037	-0.1094	0.0041	-0.3719	0.2095	408 ± 27	537 ± 83	554 ± 41	642 ± 14
210389_x_at	LOC51174	delta-tubulin	0.0002	-0.0032	0.0480	-0.2489	0.0040	137 ± 12	193 ± 19	211 ± 21	240 ± 21
219863_at	LOC51191	cyclin-E binding protein 1	0.1006	0.0000	0.0916	-0.0333	0.0077	252 ± 17	323 ± 30	336 ± 23	467 ± 73
221999_at	LOC51231	VRK3 for vaccinia related kinase 3	0.0139	-0.0004	0.0261	-0.2779	0.0000	330 ± 14	418 ± 42	369 ± 26	581 ± 24
207785_s_at	LOC51580	H-2K binding factor-2	0.4535	-0.0452	0.02753	-0.0126	0.5700	1311 ± 84	1359 ± 130	1500 ± 64	1460 ± 157
202903_at	LSM5	U6 snRNA-associated Sm-like protein	0.0173	-0.0619	0.0028	-0.0512	0.0217	109 ± 11	168 ± 20	162 ± 8	187 ± 30
220044_x_at	LUC7A	cisplatin resistance-associated overexpressed protein	0.0625	-0.0013	-0.3827	-0.0459	0.0087	1293 ± 69	1283 ± 114	1646 ± 48	1523 ± 90
210302_s_at	MAB21L2	mab-21-like 2 (C. elegans)	0.0025	0.0000	0.0734	-0.0369	0.0001	145 ± 11	188 ± 9	197 ± 16	258 ± 21
210017_at	MALT1	mucosa associated lymphoid tissue translocation 1	0.0422	-0.0071	-0.3718	-0.0078	0.0655	101 ± 12	118 ± 17	142 ± 9	145 ± 12
213705_at	MAT2A	methionine adenosyltransferase II, alpha	0.1291	-0.0001	0.0133	-0.0184	0.0038	316 ± 29	434 ± 58	490 ± 25	733 ± 13
202350_s_at	MATN2	matrin 2	0.1427	-0.0007	0.0691	-0.0218	0.0266	377 ± 45	508 ± 59	471 ± 46	634 ± 76
210136_at	MBP	myelin basic protein	0.0343	-0.0383	0.0285	-0.4138	0.2970	1624 ± 245	1962 ± 326	2352 ± 674	3195 ± 956
214057_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	0.0414	-0.0009	0.0519	-0.0378	0.0349	209 ± 16	232 ± 21	253 ± 29	314 ± 29
213761_at	MDM1	nuclear protein double minute 1	0.2852	-0.0015	0.0725	-0.0364	0.0135	315 ± 13	386 ± 26	389 ± 21	418 ± 25
213816_s_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.0087	-0.0686	0.0403	-0.2312	0.0995	136 ± 13	182 ± 30	168 ± 17	220 ± 32
203406_at	MFAP1	microfibrillar-associated protein 1	0.0001	-0.0001	0.0005	-0.0454	0.0004	877 ± 21	956 ± 44	1096 ± 20	1111 ± 58
64408_s_at	MGC4809	serologically defined breast cancer antigen NY-BR-20	0.0268	-0.0786	-0.4929	-0.0433	0.2675	65 ± 9	64 ± 9	89 ± 17	92 ± 14
206426_at	MLANA	melan-A	0.0053	-0.0574	0.0085	-0.3347	0.2505	57 ± 6	72 ± 14	83 ± 10	102 ± 27
201976_s_at	MYO10	myosin X	0.0988	-0.0457	0.0290	-0.2051	0.1025	3064 ± 290	3944 ± 556	4474 ± 301	4214 ± 576
211916_s_at	MYO1A	myosin IA	0.0123	-0.0142	-0.3886	-0.0494	0.0495	214 ± 13	229 ± 20	240 ± 13	314 ± 45
202926_at	NAG	neuroblastoma-amplified protein	0.0038	-0.0877	0.0297	-0.1395	0.1210	589 ± 40	749 ± 55	715 ± 60	787 ± 89
204528_s_at	NAP1L1	nucleosome assembly protein 1-like 1	0.0216	-0.0102	0.3438	-0.0016	0.1583	1207 ± 78	1335 ± 97	1497 ± 134	1493 ± 107
209061_at	NCOA3	nuclear receptor coactivator 3	0.2199	-0.0442	0.3014	-0.0053	0.1038	166 ± 24	218 ± 19	226 ± 12	279 ± 54
202607_at	NDST1	N-deacetylase/N-sulfotransferase 1	0.0605	-0.0342	-0.4743	-0.0392	0.0542	499 ± 57	560 ± 55	761 ± 37	644 ± 102
203961_at	NEBL	nebulette	0.0496	-0.0037	-0.4161	-0.0204	0.0710	5126 ± 259	5476 ± 442	6672 ± 660	7214 ± 975
212530_at	NEK7	NIMA (never in mitosis gene a)-related kinase 7	0.0951	-0.0165	0.3140	-0.0241	0.2232	1295 ± 132	1424 ± 170	1790 ± 261	1687 ± 165
213298_at	NFIC	nuclear factor I/C	0.0026	-0.0056	0.0037	-0.0541	0.0127	126 ± 10	158 ± 14	180 ± 8	234 ± 40
215338_s_at	NKTR	natural killer-tumor recognition sequence	0.0129	-0.1353	0.0301	-0.2544	0.0117	181 ± 13	225 ± 27	292 ± 21	234 ± 28
217844_at	NLI1F	nuclear LIM interactor-interacting factor	0.0141	-0.0102	0.0314	-0.0301	0.0436	630 ± 82	791 ± 83	1116 ± 90	1117 ± 258
205204_at	NMB	neuromedin B	0.0007	-0.0059	0.0169	0.4550	0.0383	432 ± 33	482 ± 62	492 ± 42	737 ± 139
200057_s_at	NONO	non-POU domain containing, octamer-binding	0.0360	-0.0029	-0.4987	-0.0379	0.0445	3672 ± 99	3873 ± 104	4017 ± 165	4172 ± 110
205247_at	NOTCH4	Notch homolog 4 (Drosophila)	0.1144	-0.0163	0.0329	0.4330	0.0348	302 ± 17	360 ± 40	367 ± 28	474 ± 62

Web Table 6 (6)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
220316_at	NPAS3	basic-helix-loop-helix-PAS protein	0.0759	-0.0001	0.0020	-0.1486	0.0011	427 ± 16	554 ± 44	617 ± 17	796 ± 108
217802_s_at	NUCKS	similar to rat nuclear ubiquitous casein kinase 2	0.0001	-0.0002	0.0099	-0.1530	0.0013	4406 ± 107	4549 ± 104	5193 ± 244	5660 ± 313
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	0.0008	-0.0052	0.2004	-0.0377	0.0647	740 ± 72	879 ± 74	987 ± 66	1133 ± 170
203195_s_at	NUP98	nucleoporin 98kDa	0.0044	-0.0001	0.1507	-0.0104	0.0000	97 ± 10	154 ± 25	250 ± 12	233 ± 270
210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like	0.3167	-0.0139	0.1112	-0.0072	0.1729	282 ± 34	335 ± 19	332 ± 25	399 ± 557
205301_s_at	OGG1	8-oxoguanine DNA glycosylase	0.1250	-0.0181	0.1970	-0.0363	0.0777	57 ± 7	71 ± 7	108 ± 20	103 ± 224
208735_s_at	OS4	conserved gene amplified in osteosarcoma	0.0542	-0.0290	0.0126	0.3074	0.0849	450 ± 25	483 ± 60	496 ± 27	609 ± 61
215399_s_at	OS-9	amplified in osteosarcoma	0.0037	-0.4339	0.0377	0.2597	0.4182	355 ± 24	395 ± 47	437 ± 20	415 ± 56
218304_s_at	OSBPL11	oxysterol binding protein-like 11	0.2868	-0.0153	-0.3162	-0.0412	0.2455	704 ± 69	837 ± 129	961 ± 110	993 ± 148
202553_s_at	P29	GCIP-interacting protein p29	0.0025	-0.0574	0.1144	-0.0131	0.0550	998 ± 90	1164 ± 72	1308 ± 75	1189 ± 68
220402_at	P53AIP1	p53-regulated apoptosis-inducing protein 1	0.0812	-0.0004	0.0885	-0.0401	0.0000	47 ± 9	57 ± 7	43 ± 8	125 ± 161
208113_x_at	PABPC3	poly(A) binding protein, cytoplasmic 3	0.0287	-0.1967	0.0367	-0.0759	0.3436	2272 ± 174	2625 ± 405	2907 ± 234	2622 ± 145
205719_s_at	PAH	phenylalanine hydroxylase	0.4106	-0.0367	0.1758	-0.0028	0.3914	99 ± 13	120 ± 18	121 ± 8	128 ± 6
220355_s_at	PB1	polybromo 1	0.0209	-0.0348	0.0362	-0.0008	0.0027	563 ± 20	639 ± 38	746 ± 32	650 ± 344
217739_s_at	PBEF	p18-B-cell colony-enhancing factor	0.5430	-0.0205	0.3250	-0.0138	0.2467	371 ± 34	411 ± 44	489 ± 58	499 ± 651
204476_s_at	PC	pyruvate carboxylase	0.0001	-0.0409	0.0223	-0.4650	0.1148	501 ± 40	596 ± 65	695 ± 67	713 ± 937
203845_at	PCAF	p300/CBP-associated factor	0.6531	-0.0359	0.3825	-0.0295	0.0263	1312 ± 103	1521 ± 167	2028 ± 200	1671 ± 164
204449_at	PCDH11Y	protocadherin 11 Y-linked	0.1777	-0.0450	0.0483	-0.0071	0.0645	112 ± 8	141 ± 21	125 ± 20	198 ± 36
206792_x_at	PDC1	phosducin-like	0.0431	-0.3051	0.0069	-0.0113	0.0421	175 ± 21	204 ± 11	271 ± 28	204 ± 28
216051_x_at	PDE4C	phosphodiesterase 4C	0.0069	-0.0180	0.0220	-0.1432	0.0466	4935 ± 632	6755 ± 1121	9049 ± 1345	8316 ± 1212
205137_x_at	PDGFB	platelet-derived growth factor β polypeptide	0.1198	-0.0065	0.0075	-0.0086	0.1059	376 ± 20	423 ± 60	550 ± 46	531 ± 96
205137_x_at	PDZ-73	PDZ-73 protein	0.0449	0.0000	0.1158	-0.0100	0.0004	219 ± 34	300 ± 64	385 ± 32	565 ± 65
202861_at	PER1	period homolog 1 (Drosophila)	0.0000	-0.0099	0.2052	-0.0479	0.0365	271 ± 55	393 ± 44	479 ± 50	542 ± 107
203501_at	PGCP	plasma glutamate carboxypeptidase	0.4277	-0.0302	-0.1570	-0.0239	0.2750	430 ± 57	513 ± 66	603 ± 76	556 ± 64
218387_s_at	PGLS	6-phosphogluconolactonase	0.0128	-0.0074	0.0406	0.2988	0.0540	719 ± 96	803 ± 82	880 ± 93	1140 ± 147
203445_s_at	PI4KII	phosphatidylinositol 4-kinase type II	0.0394	-0.1836	0.0255	-0.1561	0.4015	784 ± 53	835 ± 60	828 ± 52	913 ± 46
213239_at	PIBF1	progesterone-induced blocking factor 1	0.1800	-0.0210	0.3313	-0.0049	0.0412	126 ± 6	140 ± 13	132 ± 14	192 ± 29
206138_s_at	PIK4CB	phosphatidylinositol 4-kinase, catalytic, β polypeptide	0.0327	-0.0035	-0.1265	-0.0494	0.1078	1331 ± 78	1291 ± 88	1500 ± 89	1585 ± 101
205372_at	PLAG1	pleiomorphic adenoma gene 1	0.0731	-0.0015	0.0333	0.2767	0.0049	132 ± 13	121 ± 7	168 ± 20	209 ± 19
208643_s_at	PLD2	phospholipase D2	0.0072	-0.0018	0.0324	-0.0437	0.0098	332 ± 26	417 ± 33	506 ± 40	540 ± 73
202619_s_at	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0.2114	-0.0253	-0.3160	-0.0328	0.2518	251 ± 29	269 ± 40	267 ± 23	341 ± 39
208890_s_at	PLXNB2	plexin B2	0.0023	-0.0039	0.0015	-0.1719	0.0193	557 ± 42	905 ± 169	1134 ± 148	1277 ± 242
211014_s_at	PML	promyelocytic leukemia	0.1579	-0.0006	0.0436	-0.0369	0.0090	323 ± 19	352 ± 20	353 ± 15	446 ± 39
219380_x_at	POLH	polymerase (DNA directed), eta	0.0059	-0.0235	0.0199	-0.0327	0.1005	40 ± 8	51 ± 11	70 ± 17	89 ± 20
203497_at	PPARBP	PPAR binding protein	0.0989	-0.0008	0.0130	-0.0248	0.0219	219 ± 16	274 ± 16	287 ± 24	323 ± 33
208993_s_at	PPIG	peptidyl-prolyl isomerase G (cyclophilin G)	0.0083	-0.5287	0.0029	-0.0878	0.3766	518 ± 51	638 ± 50	650 ± 52	628 ± 92
201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)	0.5735	-0.0345	-0.4344	-0.0348	0.4317	1333 ± 123	1500 ± 109	1544 ± 168	1687 ± 201
204842_x_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, α	0.0028	-0.0302	0.0249	-0.2060	0.0425	709 ± 64	984 ± 147	935 ± 68	1283 ± 234
204211_x_at	PRKR	protein kinase, interferon-inducible d.s.RNA dependent	0.0103	-0.0043	0.0395	-0.0064	0.0251	246 ± 21	330 ± 33	325 ± 28	450 ± 78

Web Table 6 (7)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
205445_at	PRL	prolactin	0.4642	-0.0011	0.0380	-0.0237	0.0194	170 ± 7	198 ± 24	179 ± 5	252 ± 29
220696_at	PRO0478	PRO0478 protein	0.1663	-0.0464	0.0283	-0.0020	0.0355	69 ± 12	90 ± 12	136 ± 21	92 ± 18
202126_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.0258	-0.0201	0.0247	-0.2297	0.0927	1002 ± 53	1076 ± 41	1159 ± 63	1199 ± 72
203399_x_at	PSG3	pregnancy specific beta-1-glycoprotein 3	0.2826	-0.0111	0.1048	-0.0100	0.2034	71 ± 9	82 ± 13	76 ± 15	111 ± 18
210702_s_at	PTGIS	prostaglandin I2 (prostaglandin) synthase	0.0487	-0.0404	0.0043	-0.1266	0.0562	54 ± 9	94 ± 13	88 ± 20	126 ± 27
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1	0.0239	-0.0967	0.0116	-0.1446	0.1213	386 ± 39	521 ± 47	500 ± 62	571 ± 68
205911_at	PTHR1	parathyroid hormone receptor 1	0.0004	-0.0490	0.0360	-0.4442	0.0721	329 ± 20	454 ± 74	514 ± 48	551 ± 100
201087_at	PXN	paxillin	0.0233	-0.0361	0.1051	-0.0319	0.2670	602 ± 53	649 ± 37	735 ± 81	780 ± 88
217846_at	QARS	glutamyl-tRNA synthetase	0.0069	-0.0209	0.0046	-0.1218	0.0880	1227 ± 65	1356 ± 76	1427 ± 89	1581 ± 148
212636_at	QKI	homolog of mouse quaking QKI	0.0005	-0.0010	0.0054	-0.0078	0.0031	6635 ± 488	9010 ± 882	11099 ± 793	10982 ± 1263
220964_s_at	RAB1B	RAB1B, member RAS oncogene family	0.0197	-0.5264	0.0471	-0.0233	0.3043	814 ± 93	1084 ± 130	1187 ± 103	1010 ± 247
208730_x_at	RAB2	RAB2, member RAS oncogene family	0.0716	-0.0398	0.0827	-0.0213	0.0418	511 ± 45	627 ± 41	576 ± 78	870 ± 153
203223_at	RAB5EP	rabaptin-5	0.0111	-0.0026	0.1192	-0.0265	0.0280	64 ± 10	100 ± 14	97 ± 16	137 ± 25
204461_x_at	RAD1	RAD1 homolog (S. pombe)	0.0219	-0.1051	0.0180	0.2628	0.1006	349 ± 32	361 ± 58	481 ± 44	502 ± 75
218849_s_at	RAI	RelA-associated inhibitor	0.0013	-0.0004	0.0538	-0.0466	0.0016	328 ± 32	451 ± 31	451 ± 43	703 ± 108
209285_s_at	RAP140	KIAA1105 protein	0.0654	-0.0039	0.1381	-0.0103	0.0547	918 ± 67	1160 ± 142	1252 ± 71	1279 ± 118
219214_s_at	RBAK	RB-associated KRAB repressor	0.0374	-0.3075	0.0094	-0.4507	0.1300	117 ± 10	188 ± 18	149 ± 27	181 ± 34
205062_x_at	RBBP1	retinoblastoma binding protein 1	0.0209	-0.2634	0.0245	0.3884	0.3650	223 ± 15	230 ± 18	260 ± 16	258 ± 24
205169_at	RBBP5	retinoblastoma binding protein 5	0.0463	-0.3678	-0.3349	-0.0385	0.7640	165 ± 13	176 ± 18	179 ± 25	196 ± 27
212781_at	RBBP6	retinoblastoma binding protein 6	0.0095	-0.2117	0.0381	-0.3574	0.2409	398 ± 32	464 ± 60	506 ± 27	476 ± 38
205296_at	RBL1	retinoblastoma-like 1 (p107)	0.0004	-0.0027	0.0106	-0.0012	0.0095	41 ± 6	77 ± 11	99 ± 10	109 ± 25
213852_at	RBM8A	RNA binding motif protein 8A	-0.9563	-0.0198	0.0006	-0.1022	0.0384	1490 ± 72	1804 ± 46	1806 ± 80	1888 ± 173
219382_at	RBT1	RPA-binding trans-activator	0.0045	-0.0001	0.2426	-0.0062	0.0014	287 ± 24	334 ± 12	346 ± 20	478 ± 55
207525_s_at	RGS19IP1	regulator of G-protein signalling 19 interacting protein 1	0.0238	-0.1713	0.0105	-0.4184	0.2236	885 ± 24	1039 ± 77	1068 ± 64	1157 ± 163
206518_s_at	RGS9	regulator of G-protein signalling 9	0.0317	-0.2796	0.0287	-0.4574	0.5473	86 ± 6	110 ± 11	107 ± 23	120 ± 19
218076_s_at	RICH1	homolog of rat hadin	0.0152	-0.0003	0.2587	-0.0162	0.0030	536 ± 39	621 ± 47	614 ± 49	887 ± 99
219312_s_at	RINZF	zinc finger protein RINZF	0.0077	-0.0001	0.0269	-0.0048	0.0024	53 ± 4	64 ± 9	87 ± 9	92 ± 5
210524_x_at	RNAHP	RNA helicase-related protein	0.4991	-0.0261	0.3426	-0.0369	0.0738	3327 ± 296	4122 ± 268	3837 ± 200	5610 ± 1181
217984_at	RNASE6PL	ribonuclease 6 precursor	0.7632	-0.0432	0.0616	-0.0270	0.0356	1671 ± 133	2260 ± 119	1887 ± 199	2454 ± 283
203022_at	RNASEH2A	ribonuclease H2, large subunit	0.0821	-0.0344	0.0285	-0.3617	0.0019	262 ± 18	311 ± 37	247 ± 7	380 ± 13
211397_x_at	RNGTT	RNA guanylyltransferase and 5'-phosphatase	0.1952	-0.0283	0.0856	-0.0485	0.2043	235 ± 25	249 ± 32	336 ± 40	338 ± 69
210230_at	RNU2	RNA, U2 small nuclear	0.0326	-0.1111	0.0421	-0.3610	0.4191	164 ± 45	273 ± 83	334 ± 95	419 ± 194
214697_s_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	0.0344	-0.1326	0.0389	-0.1794	0.4233	63 ± 8	76 ± 12	67 ± 14	92 ± 17
206169_x_at	RoXan	ubiquitous tetrapeptide containing protein RoXan	0.0425	-0.0857	0.0190	-0.2736	0.1373	266 ± 33	380 ± 84	450 ± 54	399 ± 60
212933_x_at	RPL13	ribosomal protein L13	0.0008	-0.0252	0.0261	0.3873	0.0595	7513 ± 381	8578 ± 982	9468 ± 458	10087 ± 800
220113_x_at	Rpo1-2	similar to DNA-directed RNA polymerase I (135 kDa)	0.0667	-0.0032	0.0672	-0.0129	0.0427	902 ± 86	997 ± 95	1427 ± 189	1444 ± 235
214001_x_at	RPS10	ribosomal protein S10	0.0045	-0.0073	0.0594	-0.0138	0.0169	227 ± 34	364 ± 52	319 ± 29	477 ± 82
216994_s_at	RUNX2	runx-related transcription factor 2	0.0766	-0.0420	0.2358	-0.0082	0.1172	103 ± 15	136 ± 21	122 ± 20	181 ± 34
209148_at	RXRB	retinoid X receptor, beta	0.0066	-0.3866	0.0000	-0.2507	0.1774	859 ± 39	981 ± 58	1037 ± 51	975 ± 90

Web Table 6 (8)

Probe set	Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Cntrl	Incipient	Moderate	Severe
203186_s_at	S100A4	S100 calcium binding protein A4	0.2738	-0.0267	0.4680	-0.0031	0.2427	176 ± 49	270 ± 80	312 ± 62	386 ± 93
203227_s_at	SAS	sarcoma amplified sequence	0.1117	-0.0446	0.0468	-0.0322	0.1945	1098 ± 106	1315 ± 150	1433 ± 99	1431 ± 159
59705_at	SCLY	putative selenocysteine lyase	0.1838	-0.0444	0.0003	-0.0233	0.0233	108 ± 6	139 ± 12	118 ± 12	151 ± 10
221621_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	0.2649	-0.0188	0.0533	-0.0364	0.0882	135 ± 14	141 ± 10	140 ± 11	196 ± 31
201914_s_at	SEC63L	SEC63 protein	0.0650	-0.0238	0.0097	-0.4574	0.0479	230 ± 6	244 ± 25	292 ± 12	322 ± 42
203071_at	SEMA3B	semaphorin 3B	0.0018	-0.0242	0.0215	0.2637	0.0544	472 ± 63	647 ± 128	701 ± 107	1161 ± 327
213048_s_at	SET	SET translocation (myeloid leukemia-associated)	0.0357	-0.0450	0.2813	-0.0092	0.2526	2167 ± 202	2368 ± 346	2853 ± 265	2679 ± 214
33322_i_at	SFN	stratifin	0.0105	-0.0004	0.2461	-0.0059	0.0000	949 ± 44	1154 ± 24	1026 ± 46	1571 ± 140
202035_s_at	SFRP1	secreted frizzled-related protein 1	0.0007	-0.0031	0.0197	-0.0105	0.0265	47 ± 5	70 ± 8	71 ± 6	95 ± 19
201739_at	SGK	serum/glucocorticoid regulated kinase	0.5440	-0.0260	-0.2537	-0.0234	0.2301	3269 ± 434	3649 ± 399	4770 ± 682	4333 ± 684
220357_s_at	SGK2	serum/glucocorticoid regulated kinase 2	0.1788	-0.0397	0.0204	0.4107	0.0981	263 ± 11	335 ± 55	304 ± 26	400 ± 58
221519_at	SFHM3	split hand/foot malformation (ectrodactyly) type 3	0.0116	-0.0068	0.0149	-0.1847	0.0400	1267 ± 89	1570 ± 221	1781 ± 166	1963 ± 217
220937_s_at	SIAT7D	sialyltransferase 7D	0.4560	-0.0035	0.0278	-0.0050	0.0731	99 ± 8	109 ± 11	112 ± 7	130 ± 6
202782_s_at	SKIP	skeletal muscle and kidney enriched inositol phosphatase	0.6078	-0.0005	0.0337	-0.0870	0.0078	568 ± 24	568 ± 35	575 ± 36	720 ± 24
206181_at	SLAM	signaling lymphocytic activation molecule	0.2031	-0.0004	0.0027	-0.1306	0.0083	86 ± 8	127 ± 17	125 ± 11	164 ± 21
215274_at	SLC12A3	solute carrier family 12 member 3	0.1475	-0.0065	0.2175	-0.0172	0.0233	140 ± 14	174 ± 11	177 ± 25	250 ± 39
205856_at	SLC14A1	solute carrier family 14 member 1	0.0048	-0.0001	0.0407	-0.4844	0.0056	430 ± 69	517 ± 38	701 ± 91	1329 ± 326
211576_s_at	SLC19A1	solute carrier family 19 member 1	0.0195	0.0000	0.0320	-0.0004	0.0007	209 ± 19	287 ± 25	344 ± 26	426 ± 52
209865_at	SLC35A3	solute carrier family 35 member 3	0.0515	-0.0134	0.0066	-0.0023	0.0002	78 ± 7	158 ± 10	140 ± 13	156 ± 15
201073_s_at	SMARCC1	actin dependent regulator of chromatin c1	0.0162	-0.1204	-0.2783	-0.0310	0.4058	248 ± 36	293 ± 41	338 ± 19	319 ± 82
201320_at	SMARCC2	actin dependent regulator of chromatin c2	0.0011	-0.0747	0.3060	-0.0187	0.0463	932 ± 107	1146 ± 57	1502 ± 98	1293 ± 259
212152_x_at	SMARCF1	actin dependent regulator of chromatin f1	0.0206	-0.0483	0.2636	-0.0423	0.0443	1942 ± 116	2278 ± 95	2366 ± 123	2341 ± 130
201589_at	SMC1L1	SMC1 structural maintenance of chromosomes 1-like 1	0.3775	-0.0049	-0.2678	-0.0381	0.1786	620 ± 69	730 ± 100	824 ± 99	873 ± 78
207474_at	SNRK	SNF-1 related kinase	0.6988	-0.0487	0.0826	-0.0033	0.3816	60 ± 12	79 ± 12	76 ± 10	98 ± 26
220140_s_at	SNX11	sorting nexin 11	0.0211	-0.0482	0.0089	-0.2493	0.0174	436 ± 36	594 ± 52	537 ± 52	646 ± 34
219793_at	SNX16	sorting nexin 16	0.0177	-0.0954	0.3075	-0.0032	0.3081	72 ± 8	89 ± 14	101 ± 8	97 ± 16
213168_at	SP3	Sp3 transcription factor	0.4829	-0.0194	-0.3456	-0.0029	0.1453	1062 ± 49	1073 ± 103	1305 ± 74	1185 ± 103
210117_at	SPAG1	sperm associated antigen 1	0.0113	0.0000	0.0028	-0.0951	0.0005	108 ± 9	143 ± 21	142 ± 13	215 ± 18
205861_at	SPIB	SpB transcription factor (Spi-1/PU.1 related)	0.0352	-0.0016	-0.4522	-0.0102	0.0071	145 ± 14	150 ± 23	153 ± 16	241 ± 29
214072_x_at	SPUF	secreted protein of unknown function	0.5587	-0.0258	0.0221	-0.0119	0.0605	260 ± 12	331 ± 28	294 ± 19	340 ± 27
202308_at	SREBF1	sterol regulatory element binding transcription factor 1	0.0157	-0.0248	0.0002	-0.1787	0.0319	526 ± 42	967 ± 130	858 ± 105	1196 ± 268
203181_x_at	SRPK2	SFRS protein kinase 2	0.0024	-0.0078	0.2557	-0.0211	0.0249	653 ± 49	780 ± 42	898 ± 72	902 ± 75
202506_at	SSFA2	sperm specific antigen 2	0.0486	-0.0010	0.4770	-0.0126	0.0542	893 ± 105	1059 ± 103	1376 ± 188	1419 ± 174
221753_at	SSH1	slingshot 1	0.0640	-0.0177	0.1460	-0.0289	0.0711	355 ± 25	388 ± 18	427 ± 31	479 ± 50
51192_at	SSH-3	slingshot 3	0.0014	-0.0009	0.0268	-0.3388	0.0044	291 ± 21	370 ± 27	393 ± 23	619 ± 115
204964_s_at	SSPN	sarcospan (Kras oncogene-associated gene)	0.1982	-0.0037	0.3021	-0.0074	0.0230	285 ± 39	362 ± 66	426 ± 51	576 ± 98
200652_at	SSR2	signal sequence receptor, β	0.0403	-0.0640	0.0499	-0.2850	0.0660	1023 ± 47	1151 ± 63	1115 ± 26	1269 ± 101
209023_s_at	STAG2	stromal antigen 2	0.0027	-0.0085	0.3459	-0.0066	0.0240	506 ± 61	644 ± 21	837 ± 75	757 ± 122
206546_at	SYCP2	synaptonemal complex protein 2	0.0032	-0.0905	0.0001	-0.0670	0.2322	32 ± 3	45 ± 7	53 ± 7	55 ± 15

Web Table 6 (9)

Probe set Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
221276_s_at	SYNCOILIN	0.0021	-0.0021	0.3414	-0.0113	0.0160	119 ± 12	126 ± 22	165 ± 21	198 ± 18
217437_s_at	TACC1	0.2180	-0.0049	0.0210	-0.2360	0.1797	458 ± 23	501 ± 27	555 ± 54	612 ± 79
204877_s_at	TAO1	0.6842	-0.0399	0.0067	0.3208	0.0183	114 ± 10	122 ± 9	97 ± 7	180 ± 33
202133_at	TAZ	0.0666	-0.0279	0.1714	-0.0424	0.0029	475 ± 84	634 ± 95	1340 ± 265	912 ± 105
201813_s_at	TBC1D5	0.0284	-0.0129	0.0340	-0.0342	0.0431	776 ± 19	890 ± 46	925 ± 74	1062 ± 103
207554_x_at	TBXA2R	0.3649	-0.0094	0.0037	-0.1471	0.0080	171 ± 19	203 ± 20	171 ± 21	284 ± 35
212122_at	TC10	0.0055	-0.0005	0.0599	-0.0001	0.0012	154 ± 17	247 ± 26	292 ± 20	280 ± 36
209153_s_at	TCF3	0.0003	-0.0005	0.1557	-0.0216	0.0069	224 ± 32	293 ± 34	438 ± 66	468 ± 74
204043_at	TCN2	0.4467	-0.0281	0.0083	-0.0053	0.0877	239 ± 16	320 ± 30	293 ± 32	345 ± 41
202384_s_at	TCOF1	0.0040	-0.1318	0.4932	-0.0009	0.0595	150 ± 14	177 ± 18	288 ± 38	209 ± 44
201737_s_at	TEB4	0.0373	-0.0279	0.2946	-0.0212	0.0551	1927 ± 111	2131 ± 127	2717 ± 277	2452 ± 245
217853_at	TEM6	0.1228	-0.0027	0.0146	-0.2218	0.0210	2462 ± 159	2989 ± 448	4169 ± 468	4407 ± 725
204731_at	TGFBR3	0.0048	-0.0001	0.3427	-0.0168	0.0091	339 ± 33	413 ± 40	512 ± 66	630 ± 81
208104_s_at	THG-1	0.0367	-0.0213	0.0196	-0.0480	0.0386	730 ± 59	968 ± 139	1231 ± 136	1097 ± 142
222122_s_at	THO2	0.0404	-0.0989	-0.4113	-0.0364	0.2425	398 ± 39	377 ± 36	369 ± 29	470 ± 36
209154_at	TIP-1	0.0516	-0.0025	0.0013	-0.0847	0.0353	1652 ± 192	2510 ± 446	2896 ± 347	3486 ± 645
217367_s_at	TIPI1	0.0000	0.0000	0.0370	-0.0144	0.0001	511 ± 47	593 ± 47	761 ± 57	913 ± 74
210176_at	TLR1	0.0766	-0.0018	-0.3761	-0.0390	0.0162	71 ± 9	93 ± 16	100 ± 4	120 ± 7
217974_at	TM7SF3	-0.8483	-0.0293	-0.4844	-0.0116	0.4008	159 ± 16	146 ± 22	164 ± 19	193 ± 19
221882_s_at	TMEM8	0.0232	-0.5294	0.0337	-0.4415	0.5615	147 ± 13	174 ± 33	198 ± 35	227 ± 69
201645_at	TNC	0.2291	-0.0475	0.0459	-0.4827	0.0633	231 ± 46	284 ± 46	479 ± 100	391 ± 35
204932_at	TNFRSF11B	0.0240	-0.0018	0.0407	-0.1543	0.0031	48 ± 4	59 ± 6	74 ± 12	109 ± 16
207536_s_at	TNFRSF9	0.0028	-0.0428	0.0490	0.4553	0.0101	116 ± 8	173 ± 26	146 ± 7	239 ± 42
217931_at	TNRC5	0.0064	-0.0369	0.0096	-0.1251	0.0788	237 ± 16	312 ± 37	308 ± 23	403 ± 75
216333_x_at	TNXB	0.0002	-0.0121	0.0109	-0.0060	0.0003	163 ± 24	236 ± 47	451 ± 47	332 ± 55
204071_s_at	TP53BPL	0.0054	-0.0199	0.0400	-0.1030	0.0925	233 ± 9	264 ± 22	270 ± 29	324 ± 31
201691_s_at	TPD52	0.0017	-0.0030	0.0206	0.4724	0.0047	222 ± 19	263 ± 17	294 ± 28	362 ± 35
220865_s_at	TPT	0.2911	-0.0165	0.0521	-0.0410	0.0691	264 ± 21	292 ± 19	278 ± 34	362 ± 27
203568_s_at	TRIM38	0.3111	-0.0378	0.0073	-0.0026	0.3079	202 ± 19	264 ± 14	262 ± 41	292 ± 53
213968_at	TRIPAN-5	0.0358	-0.0168	0.0430	-0.0236	0.0331	82 ± 12	115 ± 12	110 ± 25	187 ± 40
208195_at	TTN	0.0050	0.0000	0.0059	-0.0187	0.0001	124 ± 12	165 ± 19	168 ± 18	286 ± 32
211460_at	TTTY9	0.0363	-0.1631	0.0267	-0.4758	0.1257	133 ± 11	195 ± 45	155 ± 12	232 ± 44
221304_at	UGT1A	0.2831	-0.0213	0.0476	-0.1752	0.0113	74 ± 9	88 ± 8	68 ± 7	123 ± 18
206094_x_at	UGT1A6	0.0845	-0.0153	0.0327	-0.4902	0.0146	200 ± 12	237 ± 37	228 ± 29	336 ± 33
208971_at	UROD	0.0146	-0.2858	0.0884	-0.0153	0.3630	373 ± 26	416 ± 32	464 ± 23	441 ± 68
202413_s_at	USP1	0.0362	-0.0028	0.2163	-0.0304	0.0367	615 ± 25	700 ± 60	818 ± 55	802 ± 66
214674_at	USP19	0.0744	-0.0118	0.0007	-0.0251	0.0021	107 ± 7	208 ± 23	184 ± 27	229 ± 23
38964_l_at	WAS	0.1578	-0.0080	0.0339	-0.2478	0.0251	1682 ± 175	2132 ± 324	1683 ± 153	2946 ± 505
210200_at	WWP2	0.0806	-0.0011	0.0066	-0.0105	0.0036	216 ± 15	268 ± 19	241 ± 18	354 ± 43

Web Table 6 (10)

Probe set Name	Description	NFT _O	MMSE _O	NFT _I	MMSE _I	ANOVA	Cntrl	Incipient	Moderate	Severe
202933_s_at	YES1	0.0385	-0.0042	0.0391	-0.0003	0.0156	609 ± 56	847 ± 86	991 ± 125	942 ± 67
210266_at	zinc-finger protein ZBRK1	0.0089	-0.1478	0.0012	-0.1152	0.0170	100 ± 8	155 ± 18	131 ± 10	158 ± 16
201369_s_at	zinc finger protein 36, C3H type-like 2	0.0119	0.0000	0.1361	-0.0031	0.0011	177 ± 26	227 ± 23	238 ± 22	409 ± 66
206240_s_at	zinc finger protein 136 (clone pHZ-20)	0.0039	0.0000	0.0098	-0.0071	0.0001	248 ± 13	321 ± 14	323 ± 30	480 ± 48
202778_s_at	zinc finger protein 198	0.0119	-0.0137	0.2370	-0.0015	0.0046	929 ± 42	961 ± 43	1140 ± 37	1030 ± 48
215948_x_at	zinc finger protein 237	0.0393	-0.0042	0.3199	-0.0229	0.0185	90 ± 8	101 ± 14	144 ± 9	133 ± 16
203247_s_at	zinc finger protein 24 (KOX 17)	0.0036	-0.0204	0.4647	-0.0326	0.1285	808 ± 84	951 ± 65	988 ± 90	1108 ± 105
206900_x_at	zinc finger protein 253	0.0950	-0.0357	0.0014	-0.0328	0.0342	203 ± 10	310 ± 33	283 ± 33	308 ± 30
206862_at	zinc finger protein 254	0.0076	-0.2379	0.1219	-0.0074	0.3517	60 ± 7	78 ± 10	76 ± 4	103 ± 36
209989_at	zinc finger protein 268	0.0017	-0.0202	0.0242	0.2564	0.0568	131 ± 11	165 ± 44	211 ± 20	238 ± 35
211975_at	zinc finger protein 289, ID1 regulated	0.0399	-0.7879	0.0395	-0.4225	0.8304	1223 ± 88	1336 ± 130	1362 ± 117	1331 ± 158
209538_at	zinc finger protein 32 (KOX 30)	0.6879	-0.0458	-0.2701	-0.0232	0.4415	418 ± 23	462 ± 85	507 ± 34	548 ± 89
206695_x_at	zinc finger protein 43 (HIF6)	0.2268	-0.0016	0.1529	-0.0241	0.0364	228 ± 15	264 ± 17	272 ± 17	310 ± 24
205089_at	zinc finger protein 7 (KOX 4, clone HF.16)	0.1458	-0.0103	-0.4816	-0.0204	0.0576	174 ± 11	185 ± 12	191 ± 11	226 ± 14
221645_s_at	zinc finger protein 83 (HPF1)	0.6657	-0.0478	0.1521	-0.0133	0.1220	283 ± 27	394 ± 44	432 ± 51	388 ± 52
204453_at	zinc finger protein 84 (HPF2)	0.0001	-0.0192	0.2051	-0.0099	0.0592	87 ± 10	96 ± 13	133 ± 19	138 ± 21
208472_at	zinc finger protein, subfamily 1A, 4 (Eos)	0.0335	-0.1455	0.0288	-0.0211	0.3678	102 ± 11	138 ± 26	121 ± 12	149 ± 34
218548_x_at	putative secreted protein ZSIG11	0.1565	-0.0164	0.0785	-0.0459	0.1738	177 ± 23	203 ± 17	207 ± 14	239 ± 20
Downregulated										
221669_s_at	acyl-Coenzyme A dehydrogenase family, member 8	-0.0048	0.0116	-0.0127	0.1005	0.0036	518 ± 21	404 ± 30	387 ± 28	376 ± 30
208637_x_at	actinin, alpha 1	-0.2078	0.0309	-0.1291	0.0461	0.0405	903 ± 46	722 ± 42	770 ± 44	720 ± 63
202135_s_at	ARP1 actin-related protein 1 homolog B, centractin β	-0.0104	0.4508	-0.0249	0.2736	0.6529	967 ± 60	860 ± 83	886 ± 62	868 ± 73
208644_at	ADP-ribosyltransferase	-0.0020	0.1298	-0.0196	-0.4561	0.1858	1196 ± 67	1111 ± 70	1092 ± 77	970 ± 60
207599_s_at	A kinase (PRKA) anchor protein 2	-0.0251	0.0691	-0.0136	-0.3125	0.2230	1219 ± 79	1193 ± 83	1141 ± 118	928 ± 129
201425_at	aldehyde dehydrogenase 2 family (mitochondrial)	-0.0615	0.0161	-0.0228	0.0997	0.0038	6579 ± 227	5151 ± 261	5117 ± 384	4890 ± 401
204174_at	arachidonate 5-lipoxygenase-activating protein	-0.0089	0.5289	-0.0055	0.3400	0.2616	771 ± 118	622 ± 75	475 ± 73	661 ± 144
202442_at	adaptor-related protein complex 3, sigma 1 subunit	-0.0012	0.0001	-0.4392	0.0096	0.0011	4853 ± 235	4193 ± 84	3928 ± 179	3611 ± 226
203527_s_at	adenomatous polyposis coli	-0.0111	0.0003	-0.1928	0.0461	0.0021	637 ± 20	511 ± 73	472 ± 57	241 ± 95
201176_s_at	archain 1	-0.0338	0.0597	-0.0229	-0.4217	0.1365	1095 ± 51	1044 ± 110	948 ± 44	814 ± 130
200734_s_at	ADP-ribosylation factor 3	-0.2452	0.0003	-0.3908	0.0486	0.0072	6169 ± 535	5151 ± 427	4503 ± 419	3636 ± 524
211891_s_at	Rho guanine nucleotide exchange factor (GEF) 4	-0.0021	0.0486	0.3604	0.0476	0.5472	461 ± 58	421 ± 40	406 ± 45	364 ± 33
210896_s_at	aspartate beta-hydroxylase	-0.0177	0.0017	-0.0265	0.2221	0.0005	561 ± 45	350 ± 40	374 ± 51	246 ± 20
208758_at	IMP cyclohydrolase	-0.0197	0.0498	-0.0028	0.1027	0.0220	1080 ± 27	987 ± 65	748 ± 99	981 ± 87
209186_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-0.0406	0.0034	0.4526	0.0301	0.0508	3230 ± 62	2685 ± 287	2553 ± 162	2404 ± 294
204966_at	brain-specific angiogenesis inhibitor 2	-0.0027	0.0614	-0.0040	0.2347	0.0029	2809 ± 219	2051 ± 120	2491 ± 244	1672 ± 149
201491_at	chromosome 14 open reading frame 3	-0.0085	0.0369	0.1424	0.0373	0.3484	1439 ± 66	1180 ± 124	1136 ± 74	1008 ± 124
222165_x_at	chromosome 9 open reading frame 16	-0.0149	0.0028	0.4553	0.0438	0.0569	1259 ± 123	1250 ± 136	1089 ± 162	914 ± 176
212252_at	calcium/calmodulin-dependent protein kinase kinase 2, β	-0.1040	0.0442	-0.1558	0.0115	0.1182	889 ± 47	825 ± 31	778 ± 96	626 ± 56
201947_s_at	chaperonin containing TCP1, subunit 2 (beta)						1961 ± 144	1737 ± 60	1436 ± 110	1562 ± 265

Web Table 6 (11)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
200910_at	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	-0.0068	0.1135	-0.0039	0.2583	0.1063	1682 ± 105	1396 ± 100	1491 ± 67	1288 ± 162
200877_at	CCT4	chaperonin containing TCP1, subunit 4 (delta)	-0.0136	0.0565	-0.2119	0.0384	0.1370	2441 ± 400	1690 ± 221	1675 ± 194	1460 ± 323
208696_at	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	-0.0357	0.4168	-0.0205	0.1860	0.1592	1481 ± 115	1170 ± 176	967 ± 43	1225 ± 251
200983_x_at	CD59	CD59 antigen p18-20	-0.0087	0.0396	-0.0258	0.2629	0.1173	1412 ± 273	1082 ± 143	1137 ± 172	663 ± 88
217881_s_at	CDC27	cell division cycle 27	-0.0232	0.0060	-0.0030	0.1676	0.0080	148 ± 15	110 ± 17	120 ± 18	58 ± 11
211297_s_at	CDK7	cyclin-dependent kinase 7	-0.0163	0.0021	-0.0137	0.0265	0.0118	219 ± 12	186 ± 9	169 ± 32	105 ± 24
219375_at	CEPT1	choline/ethanolaminephosphotransferase	-0.0185	0.0128	-0.0028	-0.4291	0.0060	636 ± 68	500 ± 83	568 ± 34	294 ± 31
204170_s_at	CKS2	CDC28 protein kinase 2	-0.0239	0.2937	-0.0140	0.1114	0.1372	225 ± 36	139 ± 12	191 ± 10	154 ± 31
205328_at	CLDN10	claudin 10	-0.0008	0.0006	-0.0275	0.0899	0.0059	1243 ± 103	975 ± 50	847 ± 137	666 ± 105
213415_at	CLIC2	chloride intracellular channel 2	-0.0493	0.0763	-0.0229	0.1437	0.0401	105 ± 30	30 ± 8	55 ± 15	24 ± 5
212358_at	CLIPR-59	CLIP-170-related protein	-0.2073	0.0011	-0.0029	0.2576	0.0076	4117 ± 165	3717 ± 244	3897 ± 334	2845 ± 184
211980_at	COL4A1	collagen, type IV, alpha 1	-0.0111	0.0357	-0.0599	0.0418	0.0339	689 ± 86	447 ± 65	423 ± 66	381 ± 79
221730_at	COL5A2	collagen, type V, alpha 2	0.0000	0.0007	-0.0116	0.0176	0.0000	1659 ± 134	724 ± 123	195 ± 45	456 ± 222
201652_at	COPS5	COP9 constitutive photomorphogenic homolog subunit 5	-0.0029	0.1119	-0.0347	0.4678	0.2415	1170 ± 60	1079 ± 167	885 ± 84	916 ± 127
201256_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	-0.0365	0.0106	0.2968	0.0477	0.0134	2624 ± 221	2158 ± 70	1833 ± 81	1970 ± 227
213846_at	COX7C	cytochrome c oxidase subunit VIIc	-0.0033	0.0009	-0.2401	0.0316	0.0021	1180 ± 99	916 ± 81	841 ± 31	748 ± 60
205630_at	CRH	corticotropin releasing hormone	-0.0235	0.0378	0.2689	0.0300	0.0581	247 ± 48	186 ± 39	108 ± 10	154 ± 21
221517_s_at	CRSP6	Sp1 transcriptional activation cofactor, subunit 6	-0.1315	0.0491	-0.0479	-0.4372	0.0973	315 ± 24	267 ± 28	228 ± 17	201 ± 54
220768_s_at	CSNK1G3	casein kinase 1, gamma 3	-0.0247	0.0095	-0.0112	0.0262	0.0277	368 ± 22	297 ± 25	303 ± 13	271 ± 30
206075_s_at	CSNK2A1	casein kinase 2, alpha 1 polypeptide	-0.0100	0.0104	-0.0453	0.2267	0.0423	431 ± 17	386 ± 20	359 ± 40	289 ± 47
203079_s_at	CUL2	cullin 2	-0.0179	0.0012	-0.2967	0.0206	0.0190	431 ± 28	382 ± 40	331 ± 17	304 ± 29
208872_s_at	DS3346	DNA segment, single copy probe LNS-CAV/LNS-CAI	-0.0304	0.0177	-0.2114	0.0005	0.1083	681 ± 58	591 ± 54	524 ± 46	495 ± 68
200033_at	DDX5	DEAD/H box polypeptide 5	-0.0471	0.5049	-0.0209	0.3871	0.6756	4816 ± 211	4787 ± 203	4361 ± 380	4314 ± 594
209407_s_at	DEAF1	deformed epidermal autoregulatory factor 1	-0.0458	0.0854	-0.0015	0.0319	0.1909	1447 ± 115	1121 ± 108	1175 ± 121	1145 ± 139
210227_at	DLGAP2	discs, large (Drosophila) homolog-associated protein 2	-0.0208	0.0009	-0.0275	0.2242	0.0238	1305 ± 73	1150 ± 147	1015 ± 128	789 ± 76
200881_s_at	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	-0.0115	0.0951	-0.0059	0.4265	0.0987	1620 ± 249	1215 ± 132	1296 ± 172	903 ± 68
212490_at	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	-0.2041	0.0408	0.2941	0.0026	0.0437	276 ± 20	215 ± 16	261 ± 22	200 ± 22
203258_at	DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	-0.0166	0.0137	-0.0392	-0.4163	0.0287	762 ± 50	617 ± 106	573 ± 57	419 ± 82
200789_at	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	-0.0045	0.0751	-0.0010	0.1452	0.2163	795 ± 40	728 ± 41	688 ± 26	651 ± 85
201632_at	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha	-0.0165	0.1292	-0.0242	0.1385	0.1055	1099 ± 39	984 ± 24	897 ± 73	920 ± 85
218488_at	EIF2B3	eukaryotic translation initiation factor 2B, subunit 1 alpha	-0.0017	0.0221	-0.0174	0.2218	0.0271	443 ± 41	406 ± 23	303 ± 13	328 ± 50
221528_s_at	ELMO2	engulfment and cell motility 2	-0.2807	0.0498	-0.3200	0.0314	0.3301	828 ± 36	772 ± 70	732 ± 67	662 ± 86
204232_at	FCER1G	Fc fragment of IgE, high affinity 1	-0.0190	0.1445	-0.0266	0.3763	0.1576	1292 ± 193	1037 ± 91	944 ± 58	921 ± 83
214505_s_at	FHL1	four and a half LIM domains 1	-0.2094	0.0486	0.3758	0.0415	0.2475	526 ± 76	515 ± 94	329 ± 38	387 ± 86
206857_s_at	FKBP1B	FK506 binding protein 1B, 12.6 kDa	-0.0074	0.0218	0.2725	0.0184	0.0794	2493 ± 299	2116 ± 186	1592 ± 196	1751 ± 286
219170_at	FSD1	fibronectin type 3 and SPRY domain-containing protein	-0.3995	0.0208	-0.0207	0.1889	0.1650	1016 ± 65	848 ± 121	823 ± 106	703 ± 101
205850_s_at	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	-0.0089	0.0515	-0.3541	0.0264	0.3529	157 ± 17	138 ± 24	111 ± 15	118 ± 26
206435_at	GALGT	UDP-N-acetyl-galactosamine	-0.0466	0.0014	0.3795	0.0130	0.0116	647 ± 76	501 ± 61	407 ± 47	388 ± 21
206662_at	GLRX	glutaredoxin (thioltransferase)	-0.0728	0.0340	-0.4513	0.0457	0.0196	1484 ± 231	829 ± 69	846 ± 76	829 ± 166

Web Table 6 (12)

Probe set	Name	Description	NFT ₀	MMSE ₀	NFT ₁	MMSE ₁	ANOVA	Cntrl	Incipient	Moderate	Severe
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthase)	-0.0324	0.0321	-0.0247	0.4324	0.0844	2336 ± 499	1694 ± 273	1658 ± 161	978 ± 281
212273_x_at	GNAS	GNAS complex locus	-0.0305	0.0024	-0.0022	0.0457	0.0151	15346 ± 513	12684 ± 969	13037 ± 942	10407 ± 1560
200744_s_at	GNB1	G protein, β polypeptide 1	-0.0362	0.2471	-0.0395	0.1740	0.1601	662 ± 73	474 ± 52	538 ± 58	482 ± 70
212288_at	GPR22	G protein-coupled receptor 22	-0.0612	0.0004	-0.2999	0.0149	0.0054	335 ± 43	240 ± 40	141 ± 30	152 ± 48
202678_at	GTF2A2	general transcription factor IIA, 2, 12kDa	-0.0174	0.1775	-0.0760	0.0448	0.1555	825 ± 39	670 ± 49	635 ± 64	683 ± 89
211569_s_at	HADHSC	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-0.2232	0.0493	-0.0326	0.4335	0.2136	323 ± 24	333 ± 17	286 ± 24	272 ± 17
211529_x_at	HLA-G	HLA-G histocompatibility antigen, class I, G	-0.0485	0.1848	-0.0247	0.2852	0.1475	1182 ± 209	823 ± 174	1040 ± 189	580 ± 158
212434_at	HMG	GrpE-like protein cochaperone	-0.0001	0.0021	-0.0204	0.2548	0.0095	548 ± 25	486 ± 57	400 ± 41	333 ± 55
208744_x_at	HSP105B	heat shock 105kD	-0.0012	0.0082	-0.0337	0.0777	0.0160	462 ± 55	309 ± 77	228 ± 37	220 ± 38
211936_at	HSPA5	HSP 570kDa	-0.0018	0.0149	-0.0090	0.1392	0.0186	2203 ± 259	1540 ± 177	1408 ± 167	1183 ± 238
218291_at	HSPC003	HSPC003 protein	-0.0072	0.0030	-0.0466	0.2915	0.0218	422 ± 16	406 ± 48	378 ± 35	284 ± 21
211969_s_at	HSPCA	heat shock 90kDa protein 1, alpha	-0.0382	0.1059	-0.0100	0.1738	0.1110	4154 ± 682	2608 ± 460	3120 ± 537	2216 ± 401
200064_at	HSPCB	heat shock 90kDa protein 1, beta	-0.0009	0.0018	-0.0232	0.0583	0.0042	8350 ± 770	5982 ± 745	5472 ± 549	4407 ± 725
214787_at	IRLB	c-myc promoter-binding protein	-0.0709	0.0048	-0.0217	0.1709	0.0004	214 ± 13	177 ± 9	207 ± 7	134 ± 15
221307_at	KCNIP1	Kv channel interacting protein 1	-0.0303	0.0362	-0.2481	0.0262	0.1303	255 ± 18	209 ± 25	201 ± 15	174 ± 38
214788_x_at	KIAA0749	KIAA0749 protein/ Dendrin	-0.0081	0.0028	-0.4395	0.0182	0.0565	3347 ± 309	3178 ± 591	2570 ± 333	1852 ± 351
209445_s_at	KIAA0905	yeast Sec31p homolog	-0.0008	0.0080	-0.0137	-0.2660	0.0108	2166 ± 81	1972 ± 97	1952 ± 102	1608 ± 156
212163_at	KIDINS220	likely homolog of rat kinase D-interacting substance	-0.0015	0.0020	-0.0208	0.0694	0.0088	2276 ± 58	2107 ± 68	1908 ± 62	1641 ± 238
209234_at	KIF1B	kinesin family member 1B	-0.0038	0.1867	-0.0227	0.2863	0.4746	5189 ± 229	4970 ± 315	4743 ± 209	4688 ± 277
203130_s_at	KIF5C	kinesin family member 5C	-0.0446	0.1471	-0.0291	0.4904	0.4423	9415 ± 336	8693 ± 827	8447 ± 608	8112 ± 467
203619_s_at	LFG	lifeguard	-0.0021	0.0067	-0.0271	-0.4897	0.0416	2634 ± 203	2468 ± 295	2140 ± 163	1807 ± 135
208936_x_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	0.0000	0.0033	-0.0256	-0.3466	0.0073	532 ± 12	528 ± 40	388 ± 35	379 ± 57
203721_s_at	LOC51096	CGI-48 protein	-0.0007	0.1188	-0.1623	0.0444	0.1178	783 ± 50	697 ± 16	621 ± 19	667 ± 83
218657_at	LOC51195	Link guanine nucleotide exchange factor II	-0.1778	0.0184	-0.0451	0.0488	0.0305	760 ± 53	459 ± 72	633 ± 128	377 ± 110
220046_s_at	LOC57018	cydin L ania-8a	-0.0176	0.5403	-0.0028	0.4446	0.1491	851 ± 54	707 ± 32	702 ± 33	755 ± 78
212741_at	MAOA	monoamine oxidase A	-0.0251	0.0034	-0.0281	0.0459	0.0208	1373 ± 102	1190 ± 59	1159 ± 76	993 ± 58
203266_s_at	MAP2K4	mitogen-activated protein kinase kinase 4	-0.0403	0.0202	-0.0292	0.1064	0.0378	1519 ± 123	1249 ± 198	936 ± 93	1072 ± 171
201475_x_at	MARS	methionine-tRNA synthetase	0.0000	0.0001	-0.0004	0.1363	0.0000	1803 ± 60	1457 ± 118	1293 ± 46	1100 ± 71
212535_at	MEF2A	MADS box transcription enhancer factor 2, polypeptide A	-0.0192	0.6612	-0.0416	-0.2256	0.4413	1536 ± 46	1513 ± 128	1675 ± 133	1375 ± 181
207098_s_at	MFN1	mitofusin 1	-0.0023	0.0158	-0.0349	-0.2853	0.0226	247 ± 13	248 ± 20	238 ± 17	175 ± 20
212945_s_at	MGA	MAX dimerization protein 5	-0.0095	0.0143	-0.0216	0.4838	0.0362	254 ± 36	219 ± 15	225 ± 36	111 ± 27
211026_s_at	MGLL	monoglyceride lipase	-0.0177	0.0033	-0.1921	0.0069	0.0667	2671 ± 109	2619 ± 222	2221 ± 173	2142 ± 133
218138_at	MKKS	McKusick-Kaufman syndrome	-0.0137	0.0019	-0.0088	0.0224	0.0006	850 ± 26	662 ± 68	568 ± 29	589 ± 52
203466_at	MPV17	MpV17 transgene, murine homolog, glomerulosclerosis	-0.0229	0.0117	-0.0429	0.3221	0.0767	315 ± 46	286 ± 69	181 ± 51	136 ± 47
218027_at	MRPL15	mitochondrial ribosomal protein L15	-0.0019	0.0002	-0.0220	0.0269	0.0001	692 ± 42	522 ± 42	394 ± 49	399 ± 32
203371_s_at	NDUFB3	mitochondrial dehydrogenase (ubiquinone) 1 β subcomplex, 3	-0.1416	0.0104	-0.0468	0.0024	0.0302	1218 ± 95	961 ± 31	1007 ± 66	877 ± 92
201226_at	NDUFB8	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 8	-0.0026	0.0001	-0.0405	0.1912	0.0007	2559 ± 119	2383 ± 192	2165 ± 199	1444 ± 95
201840_at	NEDD8	neural precursor expressed, developmentally - 8	-0.0509	0.0349	-0.0109	0.2999	0.0880	1296 ± 78	1003 ± 166	1033 ± 79	817 ± 193
206089_at	NELL1	NEL-like 1 (chicken)	-0.0574	0.0067	-0.2908	0.0448	0.0042	285 ± 72	88 ± 20	72 ± 13	50 ± 10

Web Table 6 (13)